

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 21:44:59 ; Search time 1604.11 Seconds
(without alignments)
4139.680 Million cell updates/sec

Title: US-09-786-130-32

Perfect score: 492
Sequence: 1 acaccgtctgcagcagaccac.....gcagtcacagcagcaggt 492

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: em_esthm:*
3: em_estln:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	447.4	90.9	451	9	AA311795
2	447.4	90.9	547	9	AA311795
3	395	80.3	741	10	BI824342
4	390.4	79.3	727	10	BI521608
5	388.4	78.9	785	10	BI829728
6	381	77.4	545	9	AA393182
7	379.4	77.1	530	10	BE375599
8	375.8	76.4	635	9	AL570875
9	363.6	73.9	536	9	AA393184
10	363.2	73.8	515	10	BE375685
11	360.4	73.3	531	9	AA393201
12	350.8	71.3	754	10	BE775971
13	349.4	71.0	549	9	AA393204
14	342.4	69.6	589	10	BI961303
15	328.4	66.7	901	10	BI822872
16	313.8	63.8	538	9	AA393194
17	310	63.0	463	10	BE375600

18	291.6	59.3	613	10	BI961937
19	288	58.5	401	10	BE375597
20	273.8	55.7	315	9	AA393202
21	272.2	55.3	666	10	BI153483
22	270.6	55.0	1224	11	AK009721
23	270.6	55.0	1314	11	AK003370
24	270.6	55.0	1334	11	AK008452
25	269	54.7	386	10	BE724662
26	265.4	53.9	471	9	AA393180
27	265	53.9	582	9	AA393185
28	260.4	52.9	451	9	AA393187
29	259.2	52.7	666	9	BE200246
30	250.4	50.9	685	10	BE381966
31	246.8	50.2	488	9	AA980066
32	246.8	50.2	802	10	BE684688
33	232.8	47.3	475	9	AI227465
34	192.8	39.2	473	9	BE137302
35	191.8	39.0	488	10	BE448456
36	174.6	35.5	401	10	BE920561
37	166.6	33.9	653	10	BI824811
38	160.8	32.7	431	9	AA227321
39	158.2	32.2	321	11	AK009877
40	158	32.1	321	9	AA393200
41	153	31.1	218	10	BE375598
42	145	29.5	1007	9	AV092799
43	140.2	28.5	432	9	BE200242
44	137.8	28.0	452	10	BE042057
45	129	26.2	267	9	AA393207

ALIGNMENTS

RESULT 1
AA311795
LOCUS
DEFINITION
AA311795
VERSION
AA311795.1
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
COMMENT

AA311795
451 bp
mRNA
linear
EST 19-APR-1997

Similar to Hypothetical protein C9, mRNA sequence.

Human sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fulmer,R.A., Bult
,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White
,O., Sutton,G., Blake,J.A., Brandon,R.C., Man,Wai,C., Clayton,R.A.,
Cline,T.R., Cotton,M.D., Barle-Hughes,J., Fine,L.D., Fitzgerald
,L.M., Fitzhugh,W.M., Fitchman,J.L., Geoghegan,N.S., Glodde,A.,
Guelm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M.,
Kelley,J.C., Liu,L.-I., Marrao,S.M., Merrick,J.M.,
Moreno-Palancas,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,J.F., Li,Y.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
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Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
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Wei,T.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon
,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
Venter,J.C.

Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl), 3-174 (1995)

Other ESTs: THC123801

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Journal

Medline

Comment

Fax: 3018699423
 Email: atkerlvet@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tdb/ngi/ngi.html>)
 Seq primer: M13 Reverse.

FEATURES

source
 1. 451
 /organism="Homo sapiens"
 /db_xref="ATCC (inhost):159026"
 /db_xref="taxon:9606"
 /clone_1lb="Jurkat T-cells VI"
 /cell_type="T-lymphocyte"
 /note="Vector: Bluescript SK-; Site_1: EcoRI; Site_2:
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BASE COUNT 88 a 152 c 126 g 83 t 2 others

ORIGIN

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 Best Local Similarity 99.3%; Pred. No. 2.9e-93;
 Matches 448; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

35 cctcagttagaagacaaagacccctgcccctccagcccccagttgtccagcagcta 94
 1 CCGATGTAGAGACAAAGAGACCCCTGCCCCCAGCCAGTGTCCAGCAGCTA 60
 95 agcagttccagcattggaagtgaactgagcagagtggaagtgcacatgaatgaacgc 154
 61 AGCAGTGTCCAGCATTTGGAAGTGAAGTGGCAGAGTGAAGTGCATGATGGAAGC 120
 155 tgaactatcctgtgtgctgagcagcgcttcccaacttcaagcactctactgtgtg 214
 121 TGACCTTATCTGTGTGCTGCGACCGCTTCCCACTTCAGCATCTTACTGCTGG 180
 215 gcaatgtcttccttattgagacctccagagccactgtggaaggagagacacagccgg 274
 181 GCAATGCTTCTTATTGAGACCTCCAGCGCGACTGTGGAGGGAGACACACCGGG 240
 275 aacgtggaagacagagtgacagcagctgtgcaagcctgtgtgtggaagagtcacccctg 334
 241 AACGTGGAGACAGAGTGAAGTGAAGTGGCAGAGCTTGTGCTGAGAGTGAACCCCTG 300
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 301 CCTGTGACAGACCAACTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
 395 acgtgctcctgagcagcagctgtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 454
 361 ACGTGCTCTGTGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 420
 455 cctgcccctcagacagcagcagtcacagca 485
 421 CCTGCCCTTCCAGCCACAGAGTCACAGCA 451

RESULT 2

AM962849 547 bp mRNA linear EST 01-JUN-2000
 LOCUS EST374922 MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.
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 ACCESSION AM962849
 VERSION AM962849.1 GI:8152685
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 547)
 Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt,
 I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
 Quackenbush, J.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE

Assessment of gene expression patterns in a model of colon tumor
 metastasis using a 19,200 element cDNA microarray

JOURNAL Unpublished (2000)
 COMMENT Contact: John Quackenbush
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 3528
 Fax: 301 838 0208
 Email: johnq@tigr.org
 Plate: 180

FEATURES

source
 1. 547
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_1lb="MAGE resequences, MAGE"
 /note="Vector: BluescriptSKm"

BASE COUNT 115 a 183 c 145 g 104 t

ORIGIN

Query Match 90.9%; Score 447.4; DB 9; Length 547;
 Best Local Similarity 98.7%; Pred. No. 3.1e-93;
 Matches 451; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

36 cctcagttagaagacaaagacccctgcccctccagcccccagttgtccagcagctaa 95
 1 CCGATGTAGAGACAAAGAGACCCCTGCCCCCAGCCAGTGTCCAGCAGCTA 60
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 156 gaactatcctgtgtgctgagcagcgcttcccaacttcaagcactctactgtgtgtg 215
 121 GAGCTTATCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
 216 caatgtcttccttattgagacctccagagccactgtggaaggagagacacacagccgg 275
 181 CAATGCTTCTTATTGAGACCTCCAGCGCGACTGTGGAGGGAGACACACCGGGA 240
 276 aacgtggaagacagagtgacagcagctgtgcaagcctgtgtgtggaagagtcacccctg 335
 241 ACGTGGAGACAGAGTGAAGTGAAGTGGCAGAGCTTGTGCTGAGAGTGAACCCCTG 300
 336 cctgacagacacaaactctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 395
 301 CCTGTGACAGACCAACTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
 396 cgtgctcctgagcagcagctgtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 455
 361 CGTGCTCTGTGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 420
 456 cctgcccctcagacagcagtcacagcagcaggt 492
 421 CCTGCCCTTCCAGCCACAGAGTCACAGCAACATGT 457

RESULT 3

B1824342 741 bp mRNA linear EST 04-OCT-2001
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 DEFINITION 603040762F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5181830 5',
 mRNA sequence.
 ACCESSION B1824342
 VERSION B1824342.1 GI:15935892
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 741)
 NIH-MGC <http://mgs.nci.nih.gov/>.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE

Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.

66 hrglythrGlnleucylsValalaValleuGluGlnleuThrProala 112
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 252 CAGGACGACGAGCTGTGCAAGGCGCTGTGCTGAGACGCTGACCCCTGCC 301
 113 leuHisSerThrAsnPheserCysValleuValaAspProGluGlnVala 129
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 302 CTGCACAGACCACTTTCTGTGTGCTGTGACCTGAGACAGGTGT 351
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 seq_documentation_block:
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 similar to Hypothetical protein C9, mRNA sequence.
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 451)
 Adams,M.D., Keriavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult
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 O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Claydon,R.A.,
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 L.M., Fitzhugh,W.M., Fitchman,J.L., Geoghagen,N.S., Glodok,A.,
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 Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
 Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R.,
 Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
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 Dimke,D., Feng,D.-F., Ferris,A., Fischer,C., Hastings,G.A., He,W.W.,
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 Mel,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon
 M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
 Venter,J.C.
 TITLE Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence
 JOURNAL Nature 377 (6547 Suppl.), 3-174 (1995)
 MEDLINE 96026280
 COMMENT Other_ESTs: THC123801
 Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tadb/hgi/hgi.html>)
 Seq primer: M13 Reverse
 Location/Qualifiers
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 29 CAlaAlaLysGlnCysProAlaLeuGlnValThrTrpProGluValGluV 46
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 mRNA sequence.
 ACCESSION BI824342
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 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 741)
 NIH-MGC <http://mgc.ncl.nih.gov/>,
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapds-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 21:44:59 ; Search time 1604.11 Seconds
(Without alignments)
4139.680 Million cell updates/sec

Title: US-09-786-130-32

Perfect score: 492

Sequence: 1 aacactgcctgcagcagcacc.....gcagtcacagcagcaggt 492

Scoring table: IDENTITY_NUC

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
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3: em_estin:*
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15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	447.4	90.9	451	AA311795	AA311795 EST182531
2	447.4	90.9	547	AW962849	AW962849 EST374922
3	395	80.3	741	B1824342	B1824342 603040762
4	390.4	79.3	727	B1821608	B1821608 603081449
5	388.4	78.9	785	B1829728	B1829728 603079792
6	381	77.4	545	AW393182	AW393182 CM2-ST028
7	379.4	77.1	530	BF375599	BF375599 CM2-ST028
8	375.8	76.4	635	AL570875	AL570875 AL570875
9	363.6	73.9	536	AW393184	AW393184 CM2-ST028
10	363.2	73.8	515	BF375685	BF375685 RC5-ST030
11	360.4	73.3	531	AW393201	AW393201 CM2-ST028
12	350.8	71.3	754	BG775971	BG775971 602650008
13	349.4	71.0	549	AW393204	AW393204 CM2-ST028
14	342.4	69.6	589	B1822872	B1822872 603040310
15	328.4	66.7	901	B1822872	B1822872 603040310
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18	291.6	59.3	613	10	B1961937	B1961937 MONO1_8_F
19	288	58.5	401	10	BF375597	BF375597 CM2-ST028
20	273.8	55.7	315	10	AW393202	AW393202 CM2-ST028
21	272.2	55.3	666	10	B1153483	B1153483 602915551
22	270.6	55.0	1224	11	AK009721	AK009721 Mus muscu
23	270.6	55.0	1314	11	AK008452	AK008452 Mus muscu
24	270.6	55.0	1334	11	AK008452	AK008452 Mus muscu
25	269	54.7	386	10	BF724662	BF724662 B07409.Y
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27	265	53.9	582	9	AW393185	AW393185 CM2-ST028
28	260.4	52.9	451	9	AW393187	AW393187 CM2-ST028
29	259.2	52.7	666	9	BE200246	BE200246 ug61h10.x
30	250.4	50.9	685	10	BE381966	BE381966 601271915
31	246.8	50.2	458	9	AA980066	AA980066 ua28b09.x
32	246.8	50.2	802	10	BG664688	BG664688 602798384
33	232.8	47.3	475	9	AI227465	AI227465 ufl0a03.y
34	192.8	39.2	473	9	BE137302	BE137302 ug61h10.y
35	191.8	39.0	498	10	BE448456	BE448456 ut90b07.y
36	174.6	35.5	401	10	BF920561	BF920561 QV0-NM015
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38	160.8	32.7	431	9	AW227321	AW227321 up10e06.y
39	158.2	32.2	321	11	AK009877	AK009877 Mus muscu
40	158	32.1	321	9	AW393200	AW393200 CM2-ST028
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42	145	29.5	1007	9	AV092799	AV092799 AV092799
43	140.2	28.5	412	9	BE200242	BE200242 ug61h04.x
44	137.8	28.0	432	10	BF042057	BF042057 BP250023A
45	129	26.2	267	9	AW393207	AW393207 CM2-ST028

ALIGNMENTS

RESULT 1
AA311795 451 bp mRNA linear EST 19-APR-1997
EST182531 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to
similar to Hypothetical protein C9, mRNA sequence.

ACCESSION AA311795.1 GI:1964144

VERSION EST.

KEYWORDS

ORGANISM

REFERENCE

AUTHORS

ADDITIONAL

ADDITIONAL

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Fax: 3016699423
Email: arterlavet@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES

SOURCE

Location/Qualifiers

1..451

/organism="Homo sapiens"
/db_xref="ATCC (inhost):159026"
/db_xref="taxon:9606"
/clone_lib="Jurkat T-cells VI"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 88 a 152 c 126 g 83 t 2 others
ORIGIN

Query Match 90.9%; Score 447.4; DB 9; Length 451;
Best Local Similarity 99.3%; Pred. No. 2.9e-93;

/Matches 448; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 35 cctcagttgaagacaaaggacccttgcctcccaagcccccagtggtccagcagcta 94
Db 1 cctcagttgaagacaaaggacccttgcctcccaagcccccagtggtccagcagcta 60

Oy 95 agcaggtgccagcattggaagtgaagtgccagaagtgaagtgccactgaatggaagc 154
Db 61 AGCAGTGCACAGCANTGGAAGTGAAGTGGCCAGAGTGGAAAGTGCACATGGAAGC 120

Oy 155 tgaactatcctgtgtgctcgaagcgccttcccaactcaagcactctactgtgctg 214
Db 121 TGAGCTTATCCTGTGTGCTGCGACGCCCTTCCCAACTGAGCWTCTACTGTGCTGG 180

Oy 215 gcaatgtgttccttcatltgaacccctccagccgaactgtggaaggagagaccagccgg 274
Db 181 GCAATGTTCTTCTCATTTGAGCACCCTCCAGGCCGACTGTGGAGGGAGACACCGCGG 240

Oy 275 aacgttggaagacaggtgaagcagctgtgcaagcccttgctgtagaagcagtcagccctg 334
Db 241 AACGTGGAGACAGAGTGAAGTGAAGTGGCCAGAGTGGAAAGTGCACATGGAAGC 300

Oy 335 cctgtgacagacacaactctctctgtgtgtcgtgtgagccctgaagagttgtcagcgtc 394
Db 301 CCCGTGACAGACCAACTTCTCTGTGTGCTGTGAGACCTTGAAACAGTGTGCCAGCGTN 360

Oy 395 acgtctctctgtgcccagctctgagctgtgagtggaacacttgcgcccccacaaagag 454
Db 361 ACGTGCTCTGTGGCCAGCTCTGGGCTGGGCTGAGGGCAACCTTGCCCNCCACCAAGAG 420

Oy 455 cctgtgccctccagccacagcagttccacaga 485
Db 421 CCTGTGCCCTTCCAGCCACAGAGTCCACAGCA 451

RESULT 2
AW962849 547 bp mRNA linear EST 01-JUN-2000
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AW962849 547 bp mRNA linear EST 01-JUN-2000
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE

REFERENCE
AUTHORS
TITLE

REFERENCE
AUTHORS
TITLE

JOURNAL
COMMENT

Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 180
Seq primer: Reverse.

FEATURES

SOURCE

Location/Qualifiers

1..547

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGC"
/note="Vector: pBluescriptsm"

BASE COUNT 115 a 183 c 145 g 104 t
ORIGIN

Query Match 90.9%; Score 447.4; DB 9; Length 547;
Best Local Similarity 98.7%; Pred. No. 3.1e-93;

/Matches 451; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 36 ctcagttgaagacaaaggacccttgcctcccaagcccccagtggtcccaagcagctaa 95
Db 1 CTCAGTTGAAGACAAAGAGACCCCTGCCCCCTCCAGCCCCCAGTGTCCAGCAGCTAA 60

Oy 96 gcaagttccagcattggaagtgaagtgccagaagtggaagtgaagtgccactgaatggaagc 155
Db 61 GCAGTGTCCAGCATTGGAAGTGAAGTGAAGTGGCCAGAGTGGAAAGTGCACATGGAAGC 120

Oy 156 gagcttactcctgtgtgtgctcgaagcgccttcccaactcaagcactctactgtgctg 215
Db 121 GAGCTTATCCTGTGTGCTGCGACGCCCTTCCCAACTGAGCATCTACTGTGCTGGG 180

Oy 216 caatgtgttccttcatltggaacccctccagccgaactgtggaaggagagaccagccggga 275
Db 181 CAATGTTCTTCTCATTTGAGCACCCTCCAGGCCGACTGTGGAGGGAGACACCGCGGA 240

Oy 276 acgttggaagacaggtgaagcagctgtgcaagcccttgctgtagaagcagtcagccctg 335
Db 241 ACGTGGAGACAGAGTGAAGTGAAGTGGCCAGAGTGGAAAGTGCACATGGAAGC 300

Oy 336 cctgacagacacaactctctctgtgtgtcgtgtgagccctgaagagttgtcagcgtca 395
Db 301 CCTGTGACAGACCAACTTCTCTGTGTGCTGTGAGACCTTGAAACAGTGTGCCAGCGTCA 360

Oy 396 cgtgtctctgtgcccagcctctgagctgtgagtggaacacttgcgcccccacaaagag 455
Db 361 CGTGTCTCTGTGGCCAGCTCTGGGCTGGGCTGAGGGCAACCTTGCCCNCCACCAAGAG 420

Oy 456 cctgtgccctccagccacagcagttccacagaaggt 492
Db 421 CCTGTGCCCTTCCAGCCACAGAGTCCACAGCAATGT 457

RESULT 3
B1824342 741 bp mRNA linear EST 04-OCT-2001
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

B1824342 741 bp mRNA linear EST 04-OCT-2001
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE

REFERENCE
AUTHORS
TITLE

REFERENCE
AUTHORS
TITLE

Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLAM1453 row: k column: 15
High quality sequence stop: 731.

FEATURES

Source

1. .741
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lib="IMAGE:518130"
/clone_1lib="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site.1: NotI; Site.2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

BASE COUNT 163 a 238 c 205 g 135 t

ORIGIN

Query Match

Best Local Similarity 80.3%; Score 395; DB 10; Length 741;
Matches 479; Conservative 0; Mismatches 10; Indels 8; Gaps 7;

QY 1 acacctgtctcgagaccacacagctgacatgctcagcttagaagacacaaagagcccc 60
DB 227 ACACCTGTCTCGAGACACACAGCTGCACATGCTCAGTTAGAACACAAAGAGACCCC 286
QY 61 tg-ccccccacacccccagctgttccacagagtaagcagctgtccagcatttgaaatgac 119
DB 287 TGTCCCTCCACACCCCACTGTGTCCACAGCAGTAACCACTGTCCACCAATTGGAAAGTAC 346
QY 120 ctgacagagtgtaagtgacatgtaacagctgagcttaccctgtgtgacctgac 179
DB 347 CTGGCCAGAGAGTGGAACTGCACTGAATGSAAGCTGACCTTATCCTGTGTGGCTTCAG 406
QY 180 cccgttccccaactcaagcactctactactgctgtgagcaatggttcttcaattgagcaact 239
DB 407 CCGCTTCCCAACTCAGCATCTCTACTGTGCGCAATGATGTTCCATTGAGACACT 466
QY 240 cccagagcagactgtggaagggagacccagccgggaacggtggagacaaagtacagcgc- 298
DB 467 CCCAGGCGCACTGTGGAGGGAGACCAACCGGGAACGTGGAGACACAGGTACGCAAGCT 526
QY 299 tctgcaagagctgtgtgtgagcagctgacccctgcccctgcaacagacacacttctcct 358
DB 527 TGTGCAAGGCTTGTGTCTGTGACACACTG-CCGTGCAAGCAGACCAACTTCTCTCT 585
QY 359 gttgtcgttgaacctgaaacaggtgttcacagctcagctcgtcctgacccaactc--tg 416
DB 586 GTGTGCTCGTGAGCCTGAAACAGG-TGTCCAGGTGTCACGTGTCCGGCCACCAATCATGG 644
QY 417 ggtctggctgtgagggcaactt-gccccccacccaagaagacct-gcccttcagcacaagc 474
DB 645 GCTGGGCTGTAGGGCAACTTGTGGCCCCCAACCAAGAAAGCCGTGGCCCTCCACACAGC 704
QY 475 agtcccaagcagcagcagc 491
DB 705 AGTCCACAGCAGCAGG 721

RESULT 4

BI521608 727 bp mRNA linear EST 29-AUG-2001
LOCUS 603081449F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5220396 5',
DEFINITION mRNA sequence.

ACCESSION BI521608
VERSION BI521608.1 GI:15346400
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE

1 (bases 1 to 727)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>

Plate: LLAM1554 row: b column: 13
High quality sequence stop: 685.

FEATURES

Source

1. .727
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1lib="IMAGE:5220396"
/clone_1lib="NIH_MGC_120"
/lab_host="DH10B"
/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site.1: NotI; Site.2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."

BASE COUNT 159 a 2218 c 209 g 141 t

ORIGIN

Query Match

Best Local Similarity 79.3%; Score 390.4; DB 10; Length 727;
Matches 416; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

QY 1 acacctgtctcgagaccacacagctgacatgctcagcttagaagacacaaagagcccc 60
DB 244 ACACCTGTCTCGAGACACACAGCTGCACATGCTCAGTTAGAACACAAAGAGACCCC 303
QY 61 tgccttccccaagccccagctgttccacagcagctagcagctgtccagcatttgaaatgac 120
DB 304 TGCCTCCACAGCCCCCAGCTGTGCCAGCACTGAAGAGTGTCCAGCATTTGAAAGTACG 363
QY 121 tggcagaggttgaaagtgcacactgaatgtaacgctgagctatcc-tgtgtgacctgac 179
DB 364 TGGCACAAGGTGGAAGTGCACACTGAATGAAACGCTGAGCACTTATCCGTGTGGCTTCAG 423
QY 180 cccgttccccaactcaagcactctctctgtgtgtggaatggttcttcaattgagcaact 239
DB 424 CCGCTTCCCAACTTGAACATCTCTACTGTGCGCAATGATGTTCCATTGAGACACT 483
QY 240 cccagcagactgtggaagggagacccagccgggaacggtggagacaaagtacagcagct 299
DB 484 CCCAGGCGCACTGTGGAGGGAGACCAACCGGGAACGTGGAGACACAGGTACGCAAGCT 543
QY 300 gttcgaagcctgtgtgtgagcagctgacccctgcccctgcaacagacacacacttctctg 359
DB 544 GTGCAAGGCTTGTGTCTGTGAGCAGCTGACCCCTGCGCTGCACAG-ACCAACTTCTCTGT 602

QY 360 tttgtctgttgagacccctgaacaggtgtgtcagcgttcgtctcctggcccagcttggac 419
|||||
Db 603 tttgtctgttgagacccctgaacaggtgtgtcagcgttcgtctcctggcccagcttggac 662
QY 420 tggg 423
||
Db 663 GAGG 666

RESULT 5
B1829728 785 bp mRNA linear EST 04-OCT-2001
LOCUS 603079792P1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5171399 5',
DEFINITION mRNA sequence.
ACCESSION B1829728
VERSION B1829728.1 GI:15941278
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 785)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LHAM1426 row: h column: 24
High quality sequence stop: 507.
Location/Qualifiers
1..785
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="5171399"
/clone_id="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC library."

BASE COUNT 203 a 242 c 219 g 121 t
ORIGIN

Query Match 78.9%; Score 388.4; DB 10; Length 785;
Best Local Similarity 98.3%; Pred. No. 1.4e-79;
Matches 403; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 acaccctgtctgcagaccacacagctgcacgtcctcagttagaagacaaagacccc 60
|||||
Db 72 ACACCTGTCTGCGACACACAGCTGCGACTGCTCAGTTAGAACACAAAGACCCC 131

QY 61 tggccctcccccagcccccagtttcccgacagcaggttccagcattggaagtgcac 120
|||||
Db 132 TGCCCTCCCGCCGCCAGGTGTTCCAGACAGTCCAGCATTTGGAAGTGACC 191

QY 121 tggccagagtggaagtgccacatgaatggaagcgttcacatcctgtgtgctgcagc 180
|||||
Db 192 TGCGCAGAGGTGGAAGTGCCACCTGAATGGAAGCGTGAAGCTTATCTGTGTGCTGCAGC 251

QY 181 cgcctcccccacttcagcactcctctactctggtcgtgggaatggtcttctcatctgagcacctc 240
|||||
Db 252 CCTTCCCAACTTCAGACTCTCTACTGCTGAGCAATGTTCTTCAATGAGCACCTC 311

QY 241 ccagggccagctgttgggaaggagccacagccgggaacgtggagagcagaatcagcagctg 300
|||||
Db 312 CCAGGCCGAGCTGTGGAGGGAGACACAGCCGGGAAGCTGGAGCAGAGTACGCGAGCTG 371

QY 301 tgaagccttggtctgtgagcagctgaaccctgtccctgacag-ccaccacttctctg 359
|||||
Db 372 TGCAGGCGCTGTGTGTGTGAGCAGCTGAGCCCTGCCCTCAGACAGACCACTTCTCTG 431

QY 360 tttgtctgttgagacccctgaacaggtgtgtcagcgttcagtcgtcctggccc 409
|||||
Db 432 TGTGCTGTGAGACCCGTGAACAGGTTGTCCAGCGTCACGTGCGTCTGGCC 481

RESULT 6
AM393182/c 545 bp mRNA linear EST 04-FEB-2000
LOCUS AM393182
DEFINITION CM2-ST0284-061299-046-a08 ST0284 Homo sapiens cDNA, mRNA sequence.
ACCESSION AM393182
VERSION AM393182.1 GI:6897841
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 545)
AUTHORS HCGP <http://www.ludwig.org.br/ORESTES>.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?rl=CM2&t2=CM2-ST0284-061299-046-a08&t3=1999-12-06&t4=1>)
Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence stop: 501.
Location/Qualifiers
1..545
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="ST0284"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 104 a 156 c 177 g 108 t
ORIGIN

Query Match 77.4%; Score 381; DB 9; Length 545;
Best Local Similarity 100.0%; Pred. No. 6.5e-78;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 gaagtaccctggcagagtggaagtgccacgtatggaacgtgagacttaactctgtgtg 171
|||||
Db 532 GAAGTGACCTGGCCAGAGGTGGAAGTGCCACTGAATGGAACGCTGAGCTTATCTGTGTG 473

QY 172 gccctgacgcgccttcccccaacttcacatcctactgctggtggcaatggttccttcatt 231
 |||||||
 Db 472 GCGTGCAGCGCTTCCCAACTTCACATCTCTACTGCTGGGCATGTTCTTCATT 413
 |||||||
 QY 232 gagacaccccaagccgcaactgtggaagggaagcaccagccgggaagcgtggagacaggt 291
 |||||||
 Db 412 GACACACTCCCAAGCCGACGTGTGGAGGGAGCACCAGCGGGAGACGTGGAGACACAGGT 353
 |||||||
 QY 292 accgacacttgcgaagccctgtgtgctggagagcactaacccctcctctgcacagcacaac 351
 |||||||
 Db 352 ACCGACACTGCGAAGGCTGTGGTGTGAGACACTGACCCCTGCTGCACACACCAC 293
 |||||||
 QY 352 ttcctctgtgtgctggtggaacctgaacaggtgtctcagcgtcagtcgtcctggtgcccag 411
 |||||||
 Db 292 TTCTCTGTGTGCTGTGAGCCCTGAACAAGTGTCTCAGGTACGTCTGCTGGCCAG 233
 |||||||
 QY 412 ctctggtgctggtgaggaagcaaaccttgcccccaacccaagaagccctgcctcagccac 471
 |||||||
 Db 232 CTCTGGGCTGGGCTGAGGGCAACCTTGCCCCCACCAGAGAGCCCTGCCCTCAGCCAC 173
 |||||||
 QY 472 agcaatccacagcagcagaggt 492
 |||||||
 Db 172 AGCAGTCCACAGCAGAGGT 152

RESULT 7
 BF375599/c 530 bp mRNA linear EST 24-NOV-2000
 LOCUS BF375599
 DEFINITION CM2-ST0284-061299-046-g02 ST0284 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF375599
 VERSION BF375599.1 GI:11337624
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 530)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
 Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
 ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

FEATURES
 source
 1..530
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="ST0284"
 /dev_stage="Adult"
 /note="Organ: stomach; Vector: puc18; Site:1: SmaI;
 Site:2: SmaI: A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the puc 18 vector. Reverse transcription of

BASE COUNT 95 a 152 c 169 g 114 t
 ORIGIN
 Query Match 77.1%; Score 379.4; DB 10; Length 530;
 Best Local Similarity 99.7%; Pred. No. 1.5e-77;
 Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 112 gaagtaacctgycacagagtgtgaagtgccactgaatgaacgcgtgagctatcctgtgtg 171
 |||||||
 Db 515 GAAGTACCTGGCCAGAGGTGGAAGTCCACTGAATGAACGCTGACTATCCTGTGTG 456
 |||||||
 QY 172 gccctgacgcgccttcccccaacttcacatcctactgctggtggcaatggttccttcatt 231
 |||||||
 Db 455 GCGTGCAGCGCTTCCCAACTTCAGATCTCTACTGCTGGGCAATGGTCTTCATTAT 396
 |||||||
 QY 232 gagacaccccaagccgcaactgtggaagggaagcaccagccgggaagcgtggagacaggt 291
 |||||||
 Db 395 GACACACTCCCAAGCCGACGTGTGGAGGGAGCACAACGCCGGAGACTGGGAGCACAGT 336
 |||||||
 QY 292 accgacacttgcgaagccctgtgtgctggagagcactgaacccctgcctcagccac 351
 |||||||
 Db 335 ACCGACACTGCGAAGGCTGTGGTGTGAGACACTGACCCCTGCTGCACACACCAC 276
 |||||||
 QY 352 ttcctctgtgtgctggtggaacctgaacaggtgtctcagcgtcagtcgtcctggtgcccag 411
 |||||||
 Db 275 TTCTCTGTGTGCTGTGAGCCCTGAACAAGTGTCTCAGGTACGTCTGCTGGCCAG 216
 |||||||
 QY 412 ctctggtgctggtgaggaagcaaaccttgcccccaacccaagaagccctgcctcagccac 471
 |||||||
 Db 215 CTCTGGGCTGGGCTGAGGGCAACCTTGCCCCCACCAGAGAGCCCTGCCCTCAGCCAC 156
 |||||||

QY 472 agcaatccacagcagcagaggt 492
 |||||||
 Db 155 AGCAGTCCACAGCAGAGGT 135

RESULT 8
 AL570875 635 bp mRNA linear EST 16-FEB-2001
 LOCUS AL570875
 DEFINITION AL570875 LRI_NFL006_PL2 Homo sapiens cDNA clone CSDD1012YR15 5
 prime, mRNA sequence.
 ACCESSION AL570875
 VERSION AL570875.1 GI:12927610
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 635)
 Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
 source
 1..635
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="CSDD1012YR15"
 /clone_lib="LRI_NFL006_PL2"
 /tissue_type="Placenta"
 /note="Vector: pCMVSPORT 6; Site:1: NotI; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed by
 a division of Invitrogen 9800 Medical Center Drive

High quality sequence start: 9

MEDLINE 20202663

COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=CM2&t2=CM2-ST0300-
151299-031-E04&t3=1999-12-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 44
High quality sequence stop: 60.

FEATURES
source
1..515
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0300"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT
105 a 163 c 149 g 98 t
ORIGIN

Query Match 73.8%; Score 363.2; DB 10; Length 515;
Best Local Similarity 96.5%; Pred. No. 8,1e-74;
Matches 382; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

QY 98 agtgcagcagatggaagtgacgtgagcagagtggaagtgccactgaatgaaagcgtga 157
|||
DB 3 AGAGTCAGCATGTGAAGTACCTCGCCAGATGAGTGCACATGAAATGAAAGCGTCA 62
|||
QY 158 gc-ttctctgtgtgctgcagcgcgttcccaactgaactctctactgtgtggc 216
|||
DB 63 GCGTGGTGGGTTGGCTGGCCAGCCGCTTCCCAACTTCAGCATCTCTACTGCTGGGCG 122
|||
QY 217 aatggtctctcatgtagcaacctccagcgcagctgtggaaggagagcaccagccgga 276
|||
DB 123 AATGTTCTCTCATTTAGACACCTCCAGGCGCACTGTGGAGGAGGAGACACCACTTTAA 182
|||
QY 277 cgtggagacagagtagcaagctgtgcaagcctgtgtgctgtagagcagtgaccctgac 336
|||
DB 183 CGTGGAGACACAGGTACGAGAGCTGTGCAAGGCGCTGTGCTGAGAGCAGTGCACCTGCC 242
|||
QY 337 ctgcaagaagcaccactctctctgtgtgtcgtgtgagccctgaaagagttgtcaggtcac 396
|||
DB 243 CTGCAAGACACCAACTTTTCTGTGTGTGCTGTGACCTGTGAACAGGTTGTCCAGCCTCAC 302
|||
QY 397 gtgcgtcctgagccagctctgaggtgtgaggtggaagcacccttgcccccacccaagaagac 456
|||
DB 303 GTGCTGCTGGCCAGCTCTGGGCTGGGCTGAGGGCAACTTGGCCCCCAACCAAGAGGCC 362
|||
QY 457 ctgacctcagccacagcagctcagcagcagaggt 492
|||
DB 363 CTGCTCTCCAGCCAGCAGAGTCCACAGCAGCAGAGGT 398
|||

RESULT 11
AM393201/c 531 bp mRNA linear EST 04-FEB-2000
LOCUS
DEFINITION CM2-ST0284-061299-046-f05 ST0284 Homo sapiens CDNA, mRNA sequence.
ACCESSION AM393201
VERSION AM393201.1 GI:6897860
KEYWORDS
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 531)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=CM2&t2=CM2-ST0284-
061299-046-f05&t3=1999-12-06&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 14
High quality sequence stop: 337.

FEATURES
source
1..531
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0284"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT
103 a 149 c 169 g 110 t
ORIGIN

Query Match 73.3%; Score 360.4; DB 9; Length 531;
Best Local Similarity 98.2%; Pred. No. 3.6e-73;
Matches 375; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 112 gaagtacacctgagcagagtggaagtgccactgaatgaaagcgtgaactatctgtgtg 171
|||
DB 530 GAAGTACCGCGGCAAGAGGTGGAAGTGCACCTGAATGAAACCTGAGCTTATCTGTGTG 471
|||
QY 172 gcttcagcagcgtctcccaacttaagcatctctactgtgtggaatggttccatcat 231
|||
DB 470 GCGTGCAGCGCGTTCGCCAATTCAGCATCTCTACTGCTGGGCAATGCTCTCATTT 411
|||
QY 232 gaagcactctcccaagcgcagcagct-ggagagggagacacagcgcggagaaagtgaggacaag 290
|||
DB 410 GAACACCTCCCAAGCGCAGCTGTGGAGGAGGAGACACCGCGGAAGTGGAGCAAGG 351
|||
QY 291 tacagcagctgtgcaagcctgtgtgctggaagcgtgaaccctggccctgacagcacc 350
|||
DB 350 TAGGCATCTTTTCAAGGCTTGTGCTGAGAGCAGCTGACCTGCGCTGACAGACCAA 291
|||
QY 351 ctctctctgtgtgctcgtgtgagccctgaacaggtgttcacagcgtcagctcctgtgcca 410
|||
DB 290 CTCTCTCTGTGTGCTGCTGAGACCTGTAACAGTGTGTGTCACAGCTGCTGCGGCCA 231
|||
QY 411 gctctggtgtgtgagtgaggaacctgtcccccacccaagaagcctgtgcccacagca 470
|||
DB 230 GCTCTGGGCTGGGCTGAGGGCAACTTGGCCCCCACCACCAAGAGCCCTGCTCCACCCA 171
|||
QY 471 cagcagctcacagcagcagaggt 492
|||
DB 170 CAGCAGTCCACAGCAGCAGAGGAT 149
|||

RESULT 12

Query Match	69.68;	Score 342.4;	DB 10;	Length 589;
Best Local Similarity	81.44;	Pred. No. 5.3e-69;		
Matches 397; Conservative	0;	Mismatches 91;	Indels 0;	Gaps 0;
QY	1	acacgtctccgacaccacacagctgcctcctcagttagaagacaaagacc	60	

```
/note=Organ: pooled brain, lung, testis; Vector:
PCW-SPORT6; Site_1: Noli; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
```


OM of: US-09-786-130-1 to: EST:* out_format: pfs

Date: Aug 19, 2002 11:24 PM

About: Results were produced by the Gencore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

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-MODE=framer-pzn.pool -DEV=xlh
-O=con2_1/USPFO.spool/US09786130/runat_15082002_160056_6285/app_query.fasta_1.222
-DB=EST -QFMT=fastap -SUFFIX=est -GAPOP=12.000 -GAPEXT=4.500
-MINMATCH=0.100 -LOOPEXT=0.000 -OGAPOP=4.500
-OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FCAPEXT=7.000 -YGAPEXT=10.000 -YGAPEXT=0.500 -DELCP=6.000
-DELEXT=7.000 -START=1 -MATRIX=biosum62 -TRANS=human4.0.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -HEADSIZE=500
-MINLEN=0 -MAXLEN=200000000 -USER=US09786130.@CGML_1_2515
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
-NO_XLPHY -WAIT -THREADS=1
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Search information block:

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Query: US-09-786-130-1
Query length: 164
Database: EST:*
Database sequences: 13736207
Database length: -1841457050
Search time (sec): 1601.550000
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score_list:

Sequence	Strd	Orig	ZScore	EScore	len	Documentation
gb_est1:AW962849	+	795.00	1300.33	3.5e-63	547	AW962849 EST374922 MAGE resequ
gb_est1:AA311795	+	773.00	1266.29	2.8e-61	451	AA311795 EST182531 Jurkat T-ce
gb_est1:BI824342	+	724.50	1181.06	1.5e-56	741	BI824342 603040762F1 NIH_MGC_11
gb_est1:BI829728	+	706.00	1150.01	8.3e-55	785	BI829728 603079792F1 NIH_MGC_11
gb_est1:BI521968	-	703.00	1145.93	1.4e-54	727	BI521968 603081449F1 NIH_MGC_12
gb_est1:AW933182	-	675.00	1103.08	3.4e-52	545	AW933182 CM2-ST0284-061299-046-
gb_est1:BF375599	-	670.00	1095.16	9.4e-52	530	BF375599 CM2-ST0284-061299-046-
gb_est1:AL570875	-	667.50	1089.06	2.1e-51	635	AL570875 LIT_NFL006.PH
gb_est1:AW933184	-	639.00	1044.07	6.6e-49	536	AW933184 CM2-ST0284-061299-046-
gb_est1:AW933204	-	632.00	1032.22	3.0e-48	549	AW933204 CM2-ST0284-061299-046-
gb_est1:BG775971	-	628.00	1022.32	1.1e-47	754	BG775971 602650008F1 NIH_MGC_40
gb_est1:AW933201	-	623.00	1021.16	1.2e-47	515	AW933201 CM2-ST0284-061299-046-
gb_est1:BF375685	+	623.00	1016.56	2.2e-47	515	BF375685 RCS-ST0300-151299-031-
gb_est1:BI828272	+	599.50	973.39	5.7e-45	901	BI828272 603040310F1 NIH_MGC_11
gb_est1:AW933194	-	584.00	970.04	8.7e-45	538	AW933194 CM2-ST0284-061299-046-
gb_est1:BI961303	-	546.00	952.60	1.2e-44	589	BI961303 MONO1_8.F10.b1-A005 MG
gb_est1:BF375600	-	546.00	952.79	1.8e-44	463	BF375600 CM2-ST0284-061299-046-
gb_est1:BI153483	-	519.00	844.38	8.7e-38	666	BI153483 602915551F1 NCI_CGAP_1
gb_hlc:AK009721	+	515.00	831.08	4.8e-37	1224	AK009721 Mus musculus adult ma
gb_hlc:AK003370	+	515.00	830.29	5.3e-37	1314	AK003370 Mus musculus 18 days
gb_hlc:AK008432	+	515.00	830.13	5.4e-37	1334	AK008432 Mus musculus adult ma
gb_est1:BI961937	-	512.00	813.79	3.4e-37	613	BI961937 MONO1_8.F10.g1-A005 MG
gb_est1:BE200246	-	503.00	818.07	2.5e-36	666	BE200246 ug61h10.x1 Soares_mamm
gb_est1:AW933202	+	481.00	790.17	9.1e-35	315	AW933202 CM2-ST0284-061299-046-
gb_est1:AW933180	+	479.50	783.26	2.2e-34	471	AW933180 CM2-ST0284-061299-046-
gb_est1:BE381966	+	479.50	779.13	3.8e-34	685	BE381966 601271915F1 NCI_CGAP_1
gb_est1:BF375597	-	478.50	783.40	2.2e-34	401	BF375597 CM2-ST0284-061299-046-
gb_est1:AW933187	-	478.50	773.06	8.2e-34	451	AW933187 CM2-ST0284-061299-046-
gb_est1:BG864668	+	471.00	763.41	2.8e-33	802	BG864668 602798384F1 NIH_CGAP_1
gb_est1:AA980066	+	468.50	765.49	2.2e-33	458	AA980066 ua28b09.r1 Soares_mamm
gb_est1:BF724662	+	465.00	761.62	3.6e-33	386	BF724662 bx07d09.y1 Human Tris
gb_est1:AT227465	+	443.50	727.27	2.9e-31	475	AT227465 U110a03.y1 Soares_mamm
gb_est1:AW933185	-	443.50	705.30	4.9e-30	482	AW933185 CM2-ST0284-061299-046-
gb_est1:BE448456	+	365.50	601.80	2.8e-24	498	BE448456 uc90b07.y1 Soares_mamm
gb_est1:BE137302	+	355.50	579.35	5.1e-23	473	BE137302 ug61h10.x1 Soares_mamm
gb_est1:BI824811	+	332.00	537.15	1.1e-20	653	BI824811 603033712F1 NIH_MGC_11
gb_est1:AM227321	+	308.50	503.10	8.9e-19	431	AM227321 up10e06.y1 NCI_CGAP_11
gb_est1:AK009877	+	302.50	496.49	2.1e-18	321	AK009877 Mus musculus adult ma
gb_est1:BF205051	+	299.00	488.28	6.0e-18	401	BF205051 QV0-NT0150-081100-454-
gb_est1:AW962849	-	271.00	444.70	1.6e-15	321	AW962849 CM2-ST0284-061299-046-

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gb_est1:BF375598 + 260.00 430.89 9.4e-15 218 | BF375598 CM2-ST0284-061299-
gb_est1:AV092799 + 254.00 404.12 2.9e-13 1007 | AV092799 Mus muscu
gb_est1:AA498857 + 245.50 399.12 5.5e-13 447 | AA498857 v182b02.r1 Strata
gb_est1:BE200242 - 232.50 378.65 7.6e-12 412 | BE200242 ug61h04.x1 Soares_m
gb_est1:AA297872 + 225.00 369.11 2.6e-11 320 | AA297872 EST113437 Jurkat T
```

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seq_name: gb_est1:AW962849
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seq_documentation_block:

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LOCUS AW962849 547 bp mRNA linear EST 01-JUN-2000
DEFINITION EST374922 MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.
ACCESSION AW962849
VERSION AW962849.1 GI:8152685
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
```

REFERENCE

```
1 (bases 1 to 547)
```

AUTHORS

```
Hegde,P., Ol,R., Abernathy,K., Dhara,S., Gaspar,R., Gay,C., Holt
J.E., Speed,A.I., Sharov,V., Lee,N.H., Yeaman,T.J. and
Quackenbush,J.
```

```
Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
Unpublished (2000)
```

JOURNAL

```
Contact: John Quackenbush
```

```
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
```

```
Tel: 301 838 3528
```

```
Fax: 301 838 0208
```

```
Email: johng@tigr.org
```

```
Plate: 180
```

```
Seq primer: Reverse.
```

FEATURES

```
source Location/Qualifiers
1..547
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGE"
/vector="Vector: pBluescriptSKm"
BASE COUNT 115 a 183 c 145 g 104 t
ORIGIN
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alignment_scores:

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Quality: 795.00 Length: 152
Ratio: 5.300 Gaps: 0
Percent Similarity: 98.684 Percent Identity: 98.026
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alignment_block:

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US-09-786-130-1 x AW962849 ..
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Align seg 1/1 to: AW962849 from: 1 to: 547
```

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13 seryalargserthlyaspprocyproserglnprovalphepr 29
2 TCAGTTAGAGACAAAGACCCCTGCCCTCCAGCCCAAGTTC 51
29 CALAAlAysGIncySProAlAlAeuGlValThrrProGluValGluV 46
46 alProleuAsngIyThrrLeuSerLeuSerCyValAlAcySerArpHe 62
52 AGCAGCTTAAGCAGTGTCCAGCATTTGGAAGTGCACCTGCCAGAGTGAAG 101
46 alProleuAsngIyThrrLeuSerLeuSerCyValAlAcySerArpHe 62
102 TGCCACTAATGGAACGCTGAGCTTATCTGTGTGCGCTGCAGCGCTTC 151
63 ProAsnpheSerIleLeuTyrrTrpLeuGlyAsnGlySerPheIleGluNI 79
152 CCCAACTTACAGATCCCTTACTGCTGGCAATGATGTTCTTCATGAGCA 201
79 sleuProGlyArgLeuTrpGluGlySerThrrSerArgGluArgGlySer 96
202 CCTCCAGGCGAGCTGTGGAGGAGGAGCAGCAGCGGAGACGTGGAGCA 251
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FEATURES
  source      location/Qualifiers
1. .451      1. .451
              /organism="Homo sapiens"
              /db_xref="ARCC (inhost):159026"
              /db_xref="taxon:9606"
              /clone_lib="Jurkat T-cells VI"
```

COMMENTS:
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: L1AM1453 row: k column: 15
 High quality sequence stop: 731.

FEATURES

source

Location/Qualifiers

1..741
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5181830"
 /clone_1ib="NIH_MGC_115"
 /lab_host="DH10B"
 /note="Organ: pooled brain, lung, testis; Vector:
 PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
 source anonymous pool of 6 male brains, age range 23-27; 1
 male lung, age 27; and 1 male testis, age 69. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 021. Note: this is a NIH_MGC Library."

BASE COUNT 163 a 238 c 205 g 135 t
 ORIGIN

alignment_scores:
 Quality: 724.50 Length: 168
 Ratio: 4.500 Gaps: 4
 Percent Similarity: 95.833 Percent Identity: 92.262

alignment_block:

US-09-786-130-1 x B1824342 ..

Align seg 1/1 to: B1824342 from: 1 to: 741

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1  ThrProValSerGlnThrThrAlaAlaThrAlaSerValArgSerTh 17
|||||
227 ACACCTGCTCTGCAGACACACACAGCTGCCTCAGTTAGTAGACAG 276
17  rlyAspProCys.ProSerGlnProProValPheProAlaAlaLysGln 33
|||||
277 AAAGGACCCCTGCTCCCTCCACAGCCCAAGTGTTCACGACGCTAAGCAG 326
34  CysProAlaLeuGluValThrTrpProGluValGluValProLeuAsnG1 50
|||||
327 TGTCGAGCATTTGGAAGTACCTGGGCGACAGAGTGGAAGTCCACATGATGG 376
50  yThrLeuSerLeuSerCysValAlaCysSerArgPheProAsnPheSer1 67
|||||
377 AACGCTGAGCTTATCTGCTGTGCGCTGCAGCGCTTCCCAACTTCACACA 426
67  leLeuTrpTrpLeuGluYasnGlySerPheIleGluHisLeuProGluArg 83
|||||
427 TCCTCTACTGCTGGGCAATGCTTCTTCATTGAGCAGCTCCGACGCGCA 476
84  LeuTrpGluGlySerThrSerArgGluArgGlySerThrGlyThrGln.L 100
|||||
477 CTGTGGAGGGGAGACACAGCCGGGAACGTGGAGACACAGGTACGCACACT 526
100  eucGlyValAlaLeuValLeuGluGlnLeuThrProAlaLeuHisSerThr 116
|||||
527 TGTCTCAAGGCTTGTGCTGTGAGCAGCTGCACACCTGCG.CTGCACAGCACC 575
117  AsnPheSerCysValLeuValAspProGluGlnValValGlnArgHisVal 133
|||||
576 AACCTTCTCTGTGCTGTGAGCAGCTGAACAGGT.GTCCAGCGCTCAGCT 624
133  ValLeuAlaGlnLeu.TrpAlaGlyLeuArgAlaThrLeu...ProPro 148
|||||

```

625 GTCCCGCCGACATCATGGCTGGCTTGAAGGCAACCTTGCCCCCA 674
 149 ThrGlnGluAlaLeuProSerSerHisSerSerProGlnGlnGly 164
 |||||
 675 ACCAAGAAGCCCTGGCTCCAGCAGCAGCACTCCACAGCAGCAGGG 722

seq_name: gb_est2:B1829728

seq_documentation_block:

LOCUS B1829728 785 bp mRNA linear EST 04-OCT-2001
 DEFINITION 603079792F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:517139 5',
 mRNA sequence.

ACCESSION B1829728
 VERSION B1829728.1 GI:15941278

KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.

REFERENCE
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL

COMMENT

Email: c9apbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: L1AM1426 row: h column: 24
 High quality sequence stop: 507.

FEATURES

source

Location/Qualifiers

1..785
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5171399"
 /clone_1ib="NIH_MGC_119"
 /tissue_type="medulla"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: PCMV-SPORT6; Site_1: NotI;
 Site_2: EcoRV (destroyed); RNA source normal medulla from
 anonymous male age 27. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.3 kb, insert size range
 0.9-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 013. Note:
 this is a NIH_MGC Library"

BASE COUNT 203 a 242 c 219 g 121 t
 ORIGIN

alignment_scores:
 Quality: 706.00 Length: 178
 Ratio: 4.555 Gaps: 4
 Percent Similarity: 87.079 Percent Identity: 80.899

alignment_block:

US-09-786-130-1 x B1829728 ..

Align seg 1/1 to: B1829728 from: 1 to: 785

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|||||
72 ACACCTGCTCTGCAGACACACACAGCTGCCTCAGTTAGTAGACAC 121
17  rlyAspProCysProSerGlnProProValPheProAlaAlaLysGln 34
|||||
122 AAAGGACCCCTGCTCCCTCCGCGCCGAGTGTTCACAGCAGCTAAGCAGT 171

```

```
34 yspProAlaLeuGluValThrTrpProGluValGluValProLeuAsnGly 50
|||||
172 GTCCAGCATTTGGAATGACCTGGCCAGAGGTGGAAAGTGCACATGAATGA 221
51 ThrLeuSerLeuSerCysValAlaCysSerArgPheProAsnPheSer11 67
|||||
222 ACCCTGAGCTTATCTGTGTGGCTGACGCCGTCCCAACTTCACACAT 271
67 eLeuTyTrpLeuGlyAsnGlySerPheLeuHisLeuProGlyArgL 84
|||||
272 CCTCTACTGGCTGGGCAATGTTCTTCATTGACACCTCCAGCGCGAC 321
84 eutTrpGluGlySerThrSerArgGluArgGlySerThrGlyThrGlnLeu 100
|||||
322 TGTGGGGGGGGAGACACCGCGGGAACGTGGAGACAGGTACGACGCTG 371
101 CysLeuValAlaLeuValLeuGluGlnLeuThrProAlaLeuHisSerThrA 117
|||||
372 TGCAGAGCCTTGGTGCTGGAGACAGTGCACCTGCGCTGCACAGACCA 421
117 snPheSerCysValLeuValAspProGluGlnValValGlnArgHisVal 133
|||||
422 ACTTCTCCTGTGTGTGTGGACCTGGAACAGTTGTCCAGCGTCACGTC 471
134 ValLeuAlaGlnLeuTrpAlaGlyLeuArg..... 143
|||||
472 GGTCTGGGCCCAAGCTGTGAGCGCTGGAGGCGCAAAACCTTGCGCC 521
144 .....AlaThrLeuProProThrGlnGlnAlaLeuPro 154
|||||
522 CCCGCAAGCCAAAGAAATGCCACTTGGCCCCCTCCCAAGGACAGAGGAC 571
155 SerSerHisSerSerProGlnGlnGly 164
::: ::::: :::::
572 GGGATTACACACAGAAAGACCAAAATGGC 601
seq_name: gb_est2:BI521608

seq_documentation_block:
LOCUS BI521608 727 bp mRNA linear EST 29-AUG-2001
DEFINITION 60308149P1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5220396 5',
ACCESSION BI521608
VERSION BI521608.1 GI:15346400
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 727)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: LHAM1554 row: b column: 13
High quality sequence stop: 685.
Location/Qualifiers
1..727
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="5220396"
/clone_id="NIH_MGC_120"
/lab_host="DH10B"
/note="Organ: pooled pancreas and spleen; Vector:
pcmv-sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
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source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH-MGC library."
BASE COUNT 159 a 218 c 209 g 141 t
ORIGIN

alignment_scores:
Quality: 703.00 Length: 150
Ratio: 4.916 Gaps: 1
Percent Similarity: 95.333 Percent Identity: 92.667

alignment_block:
US-09-786-130-1 x BI521608 ..
Align seg 1/1 to: BI521608 from: 1 to: 727

1 ThrProValSerGlnThrThrAlaAlaThrAlaSerValArgSerTh 17
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244 ACACCTGTCTGCGACACACACACAGCTGCCACTGCTCAGTTGAAGCAC 293
17 rlyAspProCysProSerGlnProValPheProAlaAlaLysGlnC 34
|||||
294 AAGAGACCCCTGCCCTCCAGCCCAAGTGTCCAGCAGTAACAGT 343
34 yspProAlaLeuGluValThrTrpProGluValGluValProLeuAsnGly 50
|||||
344 GTCCAGCATTTGGAATGACCTGGCCAGAGGTGGAAAGTGCACATGAATGA 393
51 ThrLeuSerLeuSerCysValAlaCysSerArgPheProAsnPheSer1 67
|||||
394 ACCCTGAGCTTATCTGTGTGGCTGACGCCGTCCCAACTTCACACAT 443
67 lLeuTyTrpLeuGlyAsnGlySerPheLeuHisLeuProGlyArgL 83
|||||
444 TCCTCTACTGGCTGGGCAATGTTCTTCATTGACACCTCCAGCGCGCA 493
84 LeuTrpGluGlySerThrSerArgGluArgGlySerThrGlyThrGlnLeu 100
|||||
494 CTGTGGAGGGGAGACACACACCGGGAACGTGGAGACAGTAACGACGCT 543
100 uCysLeuAlaLeuValLeuGluGlnLeuThrProAlaLeuHisSerThrA 117
|||||
544 GTCCAGAGCCTTGGTGCTGGAGACAGTGCACCTGCGCTGCACAG. ACCA 592
117 snPheSerCysValLeuValAspProGluGlnValValGlnArgHisVal 133
|||||
593 ACTTCTCCTGTGTGTGTGGACCTGGAACAGTTGTCCAGCGTCACGTC 642
134 ValLeuAlaGlnLeuTrpAlaGlyLeuArgAlaThrLeuProProThr 149
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643 GTCTTGGCCAGCTGTGGGTGAGGACCAAGGAGAGGCTCCAGGACNA 690
seq_name: gb_est1:AW393182

seq_documentation_block:
LOCUS AW393182 545 bp mRNA linear EST 04-FEB-2000
DEFINITION CM2-ST0284-061299-046-a08 ST0284 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW393182
VERSION AW393182.1 GI:6897841
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 545)
HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
unpublished (1999)
```


COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&tl2=CM2-ST0284-
061299-046-208&tl3=1999-12-06&tl4=1)
Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence stop: 501.
Location/Qualifiers
1. 545
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0284"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 104 a 156 c 177 g 108 t
ORIGIN

alignment_scores:
Quality: 675.00 Length: 127
Ratio: 5.315 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-786-130-1 x AM393182/rev ..

Align seg 1/1 to reverse of: AM393182 from: 1 to: 545

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38  GUUAlrhrtrpprogluValGluValProleuansnglythrleuSerle 54
|||||
532 GAAGTGACCTGGCCAGAGTGGAAGTGCACATGAGACGCTGAGCTT 483
|||||
54  uSerCysValAlaCysSerArgpneProAsnPheserlleuTyrrPL 71
|||||
482 ATCCGTGTGGCCTGCACCGCTTCCCACTTCAGCATCCTCTACTGGC 433
|||||
71  euGLyAsnGLySerPheIleGLuHisleuProGLyArgleuTrpGLnGLy 87
|||||
432 TGGGCAATGGTCTTCTTCAATTAGACACCTCCAGGCGGAGTGGGAGGG 383
|||||
88  SerThrSerArgGluArgGlySerThrGlyThrGlnleuCysLysAlaLe 104
|||||
382 AGCACACACCGGGAACGTGGGAGCAGAGTACGAGCTGTGCAAGGCTT 333
|||||
104 uValleuGLnleuThrProAlaLeuHisSerThrAsnPheserCysV 121
|||||
332 GGTGCTGGAGAGCTGACCCCTGCCCTGCACAGACCAACTTCTCTCTGTG 283
|||||
121 allleuValAspProGLnleuValValGlnArgHisValValleuAlaGln 137
|||||
282 TGCTGTGTGACCTGTGACAGAGTGTGCCAGCTCACGTCTGTGCCCCAG 233
|||||
138 LeuTrpAlaGlyLeuArgAlaThrLeuProProThrGlnGlnAlaLeuPr 154
|||||
232 CTGTGGGCTGGGCTGAGGGCAACCTTGCCCCCAACCAAGAGCCCTGCC 183
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154 uSerSerHisSerSerProGlnGlnGlnGly 164
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182 CTCAGGCCACAGAGTCCACAGCAGCAGAGGT 152

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seq_name: gb_est2:BF375599

seq_documentation_block:

LOCUS BF375599 530 bp mRNA linear EST 24-NOV-2000
DEFINITION CM2-ST0284-061299-046-g02 ST0284 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF375599
VERSION BF375599.1 GI:11337624
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 530)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
CONTACT: Simpson A.J.G.

COMMENT Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&tl2=CM2-ST0284-
061299-046-g02&tl3=1999-12-06&tl4=1)
Seq primer: puc 18 forward
High quality sequence start: 10
High quality sequence stop: 58.
Location/Qualifiers

FEATURES

source

1. 530

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0284"
/dev_stage="Adult"

/note="Organ: stomach; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 95 a 152 c 169 g 114 t

ORIGIN

alignment_scores:
Quality: 670.00 Length: 127
Ratio: 5.276 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.213

alignment_block:
US-09-786-130-1 x BF375599/rev ..

Align seg 1/1 to reverse of: BF375599 from: 1 to: 530

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38  GUUAlrhrtrpprogluValGluValProleuansnglythrleuSerle 54
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515 GAAGTGACCTGGCCAGAGTGGAAGTGCACATGAGACGCTGAGCTT 466
|||||
54  uSerCysValAlaCysSerArgpneProAsnPheserlleuTyrrPL 71
|||||
465 ATCCGTGTGGCCTGCACCGCTTCCCACTTCAGCATCCTCTACTGGC 416
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71  euGIyasnGIySerPheIIeGIuHISLeuProGIyArGIeUTrPGIuGIy 87
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415  TGGGCAATGTTCTTCATTGAGCACCTCCACAGCCGACACTGTGGAGGG 366
   |||||||
88  SerThSerArgIuArGIySerThrNGIyThrGIuLeuCySISySAlaE 104
   |||:::|||||
365  AGCAACAGCGGGAGCTGGGACACAGTACGACACTGTGCAGAGCCTT 316
   |||||||
104  uVAlleuGIuGIuLeuThrProAlaLeuHISerThrAsnPheSerCysV 121
   |||||||
315  GGTGCTGAGACACTGACCCCTGCTGCACACACCACTTCTCCTGTG 266
   |||||||
121  aIleuValAspProGIuGIuValaIGIuArGIHISyValIleuAlaGIu 137
   |||||||
265  TGCCTGTGACCTGTGAACAGGTGTGCAGGCTGCCTGCTGGCCAG 216
   |||||||
138  LeuTrAlaGIyLeuArGIaThrLeuProProThrGIuGIuAlaLeuP 154
   |||||||
215  CTCTGGGCTGGGCTGAGGGCACCTTGCCCCACCCCAAGAGCCCTTGC 166
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154  oSerSerHISerSerProGIuNGIuNGIy 164
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165  CTCACGACAGCAGCTCCACAGCAGAGGT 135

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seq_name: gb_est1:AL570875

seq_documentation_block:

LOCUS AL570875 635 bp mRNA linear EST 16-FEB-2001
 DEFINITION AL570875 LTI_NFL006.PL2 Homo sapiens cDNA clone CS0D1012YF15 5
 prime, mRNA sequence.

ACCESSION AL570875
 VERSION AL570875.1 GI:12927610

KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 635)

AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France

Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr.
 Location/Qualifiers

FEATURES

source

1..635

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CS0D1012YF15"

/clone_lib="LTI_NFL006.PL2"

/tissue_type="Placenta"

/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed by
 Life Technologies. Contact : Feng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"

BASE COUNT

128 a 213 c 170 g 118 t 6 others

ORIGIN

alignment_scores:

Quality: 667.50 Length: 154

Ratio: 4.635 Gaps: 2

Percent Similarity: 93.506 Percent Identity: 91.558

alignment_block:

US-09-786-130-1 x AL570875 ..
 Align seg 1/1 to: AL570875 from: 1 to: 635

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1  ThrProValSerGIuThrThrThrAlaAlaThrAlaSerValaArgSerTh 17
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175  ACACCTGTCTCGCAGACACACACAGCTGCCAGCTGCCTCAGTTAAGAAC 224
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17  rIySAsp...ProCysProSerGIuProProValaPheProAlaAlaLysG 33
   |||:::|||||
225  AAGAGACMCCCTCGGCCCTCCACAGCCCACTGTTCCACAGCAGTAAAG 274
   |||||||
33  IncysProAlaLeuGIuValaThrTrpProGIuValaGIuValaProLeuAsn 49
   |||||||
275  AGTGTCCAGATTGGAAGTACCTGGCCAGAGGTGAAGTGCACACGAAT 324
   |||||||
50  GIYThrLeuSerSerSerCysValaIaCysSerArgPheProAsnPheS 66
   ||| |||||||
325  GGACG.CTGAGCTTATTCCTGTGTGGCTTGCAGCCGCTTCCCAACTTCAG 373
   |||||||
66  rIleuTyTrpLeuGIyAsnGIySerPheIIeGIuHISLeuProGIyA 83
   |||||||
374  CATCTCTACTGGCTGGGCAATGTTCTTCATTGAGCACCTCCAGGCC 423
   |||||||
83  rGIeUTrPGIuGIySerThrSerArgGIuArGIySerThrGIyThrGIu 99
   |||||||
424  GACTGTGGAGGGGAGCACACCGGGGAACGTGGGAGCACAGGTAGCAG 473
   |||||||
100  LeuCySISyAlaLeuValleuGIuGIuGIuLeuThrProAlaLeuHISerTh 116
   |||||||
474  CTGTGCAGAGGCTTGTGCTGTGCAGACAGCAGCCCGGCCGNCACACAC 523
   |||||||
116  rAsnPheSerCysValaLeuValaAspProGIuGIuValaIGIuArGIHISy 133
   |||||||
524  CAACCTCTCCTGTGTGTGCTGTGGGAGCTGACACAGTT.GTCCAGCGTCAG 572
   |||||||
133  aIleuValaGIuGIuLeuThrPala.GIYleuArGIaThrLeuProProTh 149
   |||||||
573  TCGTCTTGCCGACGCTGTGGGCTTAGGGTTGAGGGCAACTTGTGCCCCAC 622
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149  rGIuGIuAla 152
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623  CCAGAGAGCC 632

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seq_name: gb_est1:AW393184

seq_documentation_block:

LOCUS AW393184 536 bp mRNA linear EST 04-FEB-2000
 DEFINITION CW2-ST0284-061299-046-all ST0284 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW393184
 VERSION AW393184.1 GI:6897843

KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 536)

AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
 TITLE The FAPESP/LICR Human Cancer Genome Project
 JOURNAL Unpublished (1999)

COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?cli-CM2&t2-CM2-ST0284-

061299-046-all&t3-1999-12-06&t4-1)

Seq primer: puc 18 forward

High quality sequence start: 9
High quality sequence stop: 536.
Location/Qualifiers
1..536

FEATURES
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0284"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site:1: Sma1;
Site:2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 105 a 150 c 172 g 109 t
ORIGIN

alignment_scores:
Quality: 639.00 Length: 128
Ratio: 5.112 Gaps: 1
Percent Similarity: 97.656 Percent Identity: 96.875

alignment_block:
US-09-786-130-1 x AM393184/rev ..

Align seg 1/1 to reverse of: AM393184 from: 1 to: 536

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38 GluValAlhTrTPProGluValAGluValProLeuAsnGlyThrLeuSerLe 54
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521 GAACTGACCTGGCCAGAGCTGGAAGTCCACTGAATGAGACGCGAGCTT 472
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54 uSerCysValAlaCysSerArgPheProAsnPheSerIleLeuTyrTrp 71
   |||||||
471 ATCTGTGTGGCTGCACAGCCGCTTCCCACTGACATCTCTCACTGTC 422
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71 euGlyAsnGlySerPheIleGluHisLeuProGlyArgLeuTrpGluGly 87
   |||||||
421 TGGGCATATGCTTCTTCATTAGACACCTCCAGGCCAGACTGTGGAGGG 372
   |||||||
88 SerThrSerArgGluArgGlySerThrGlyThrGln.LeuCysLysAla 104
   |||||||
371 AGCACACGACCCGGGAACGTGGGAGCACAGGTACGACGCTTGTCAAGGCT 322
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104 euValLeuGluGlnLeuThrProAlaLeuHisSerThrAsnPheSerCys 120
   |||||||
321 TGGTTCTGGAGCAGCTGACCCCTGCTGCACACGACCAACTTCTCTCT 272
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121 ValLeuValAspProGluGlnValValGlnArgHisValValLeuAlaG 137
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271 GTGCTGTGGAGCCTGAACAGGTGTCCAGAGTCACGTCGTCGGGCCA 222
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137 nLeuTrpAlaGlyLeuArgAlaThrLeuProProThrGlnGluAlaLeu 154
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221 GCTTGTGGGCTGGGCTGAGGGCAACCTTGCCGCCACCAAGAACCCCTGC 172
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154 roSerSerHisSerSerProGlnGlnGlnGly 164
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171 CCTCCAGCCACAGCATCCACAGCAGCAGGGT 140

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seq_name: gb_est1:AM393204

seq_documentation_block:

LOCUS AM393204 549 bp mRNA linear EST 04-FEB-2000
DEFINITION CM2-ST0284-061299-046-906 ST0284 Homo sapiens cDNA, mRNA sequence.
ACCESSION AM393204
VERSION AM393204.1 GI:6897863
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 549)
AUTHORS HCGP <http://www.ludwig.org.br/ORESTES>.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT

Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2<2=CM2-ST0284-061299-046-906<3=1999-12-06<4=1>)
Seq primer: puc 18 forward
High quality sequence start: 20
High quality sequence stop: 71.
Location/Qualifiers

FEATURES
source

1..549
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0284"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site:1: Sma1;
Site:2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 108 a 154 c 175 g 112 t
ORIGIN

alignment_scores:
Quality: 632.00 Length: 129
Ratio: 5.056 Gaps: 2
Percent Similarity: 96.899 Percent Identity: 96.124

alignment_block:
US-09-786-130-1 x AM393204/rev ..

Align seg 1/1 to reverse of: AM393204 from: 1 to: 549

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38 GluValAlhTrTPProGluValAGluValProLeuAsnGlyThrLeuSerLe 54
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520 GAACTGACCTGGCCAGAGCTGGAAGTCCACTGAATGAGACGCTGAGCTT 471
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54 uSerCysValAlaCys.SerArgPheProAsnPheSerIleLeuTyrTrp 70
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470 ATCTGTGTGGCTGCACAGCCGCTTCCCACTGACATCTCTCACTGTC 421
   |||||||
71 euGlyAsnGlySerPheIleGluHisLeuProGlyArgLeuTrpGluGly 87
   |||||||
420 CTGGGCATATGCTTCTTCATTAGACACCTCCAGGCCAGACTGTGGAGGG 371
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87 ySerThrSerArgGluArg.GlySerThrGlyThrGlnLeuCysLysAla 103
   |||||||
370 GAGCACACGACCCGGGAACGTGGGAGCACAGGTACGACACTTTCGAAGGCC 321
   |||||||
104 LeuValLeuGluGlnLeuThrProAlaLeuHisSerThrAsnPheSerCys 120
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320 TTGGTGTGGAGCAGCTGACTGCTGCTGCACAAACCAACTTCTCTCTG 271
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120 sValLeuValAspProGluGlnValValGlnArgHisValValLeuAlaG 137
   |||||||
270 TGTGCTGTGGAGCCTGAACAGGTGTTCACAGTCGTCGTCGGGCC 221
   |||||||
137 nLeuTrpAlaGlyLeuArgAlaThrLeuProProThrGlnGluAlaLeu 153
   |||||||
220 AGCTGTGGGCTGGGCTGAGGGCAACCTTGCCGCCACCAAGAACGCCCTG 171

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154 ProSerSerHisSerSerProGlnGlnGlnGly 164
|||||
170 CCTCCAGCCACAGCAGCAGCAGCAGCAGG 138

seq_name: gb_est2:B6775971

seq_documentation_block:
  LOCUS      B6775971          754 bp      mRNA      linear      EST 15-MAY-2001
  DEFINITION  602650008F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:4761073 5',
  mRNA sequence.
  ACCESSION  B6775971
  VERSION    B6775971.1 GI:14046288
  KEYWORDS   EST.
  SOURCE      human.
  ORGANISM   Homo sapiens
              Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
  REFERENCE  1 (bases 1 to 754)
              NIH-MGC http://mgc.nci.nih.gov/.
  AUTHORS    National Institutes of Health, Mammalian Gene Collection (MGC)
  TITLE      Unpublished (1999)
  JOURNAL    Contact: Robert Strausberg, Ph.D.
              Email: cgaaps-remail.nih.gov
  COMMENT    Tissue Procurement: DCTD/DTF
              CDNA Library Preparation: Ling Hong/Rubin Laboratory
              CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
              DNA sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LNL at:
              http://image.llnl.gov
              Plate: L10M1612 row: p column: 02
              High quality sequence stop: 653.
              Location/Qualifiers
                1..754
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:4761073"
                /clone_lib="NIH_MGC_40"
                /tissue_type="carcinoma, cell line"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: prostate; Vector: pOT7; Site_1: XhoI;
                Site_2: EcoRI; cDNA made by oligo-dT priming.
                Directionally cloned into EcoRI/XhoI sites using the
                following 5' adaptor: GGCACGAG(G). Library constructed by
                Ling Hong in the laboratory of Gerald M. Rubin (University
                of California, Berkeley) using ZAP-CDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies).
                Note: this is a NIH_MGC Library."
  BASE COUNT  174 a      242 c      196 g      142 t
  ORIGIN

alignment_scores:
  Quality:      628.00      Length:      155
  Ratio:        4.361      Gaps:      3
  Percent Similarity: 92.903      Percent Identity: 90.968

alignment_block:
  US-09-786-130-1 x B6775971 ..

Align seg 1/1 to: B6775971 from: 1 to: 754

1  ThrProValSerGlnThrThrThraAlaAlaThraAlaSerValArgSerTh 17
|||||
185 ACACCTGCTGCAGACACACACACAGCTGCCTCCTCAGTTAAGAACAC 234

17  rLysAspProCysProSerGlnProProValAlaPheProAlaAla..LysG 33
|||||
235 AAAGACACCCCTGCCCTCCAGCCCAAGTGTCCACAGAGCTAAGGCA 284

33  ncysProAlaLeuGluValThrTirProGluValGluValProLeuAsng 50
|||||
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```
285 GTGTCCAGCATTTGGAAAGTACCTGGCCAGAGGTGCAATGCCACTGATG 334
50  lYThrLeuSerLeuSerCysValAlaCysSerArgPheProAsnPhSer 66
|||||
335 GAACGCTGAGCTTATTCCTGTGTGGCTGCAGCGG..TTCCCAACTTCAC 383
67  lLeuTyTTrPleuGlnGlnGlnGlnSerPheIlleGlnHisLeuProGly 83
|||||
384 ATCCCTTACTGCTGGCGCAATGATTCCTTCATTGACACCTCCACAGCCA 432
83  gleuTrpGluGlnGlnSerThrSerArgGluArgGlnGlnSerThrGlyThrGln 100
|||||
433 .CTGTGGAGGGAGGACACCAACCGGGAACCTGGAGACACAGTACGACAC 482
100 euCysLysAlaLeuValLeuGlnGlnLeuThrProAla...LeuHisSer 115
|||||
483 TGTGCAAGGC..TTGGTGTGGAGACAGCTGACACCTTGACCTGCACAC 531
116 ThrAsnPhSerCysValLeuValAspProGluGlnValValGlnArg.. 131
|||||
532 ACCAACTTCTCCTGTGTGCTGCGACCTGAAACAGGTGTCCAGGCTCA 581
132 .HisValValLeuAlaGlnLeuThrPalGlnLeuArgAlaThrLeuProp 148
|||||
582 ACGTCCGCTCTGCGCCACACTGTGGCTGGATGAGGGCAACTTGCCCC 631
148 roThrGlnGlnAla 152
|||
632 CACACCAAGACGC 645

seq_name: gb_est1:AM393201

seq_documentation_block:
  LOCUS      AM393201          531 bp      mRNA      linear      EST 04-FEB-2000
  DEFINITION  CM2-ST0284-061299-046-f05 ST0284 Homo sapiens cDNA, mRNA sequence.
  ACCESSION  AM393201
  VERSION    AM393201.1 GI:6897860
  KEYWORDS   EST.
  SOURCE      human.
  ORGANISM   Homo sapiens
              Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
  REFERENCE  1 (bases 1 to 531)
              HCGP http://www.ludwig.org.br/ORESTES.
  AUTHORS    The FAPESP/LICR Human Cancer Genome Project
  TITLE      Unpublished (1999)
  JOURNAL    Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
  COMMENT    This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&t2=CM2-ST0284-
              061299-046-f05&t3=1999-12-06&t4=1)
  Seq primer: puc 18 forward
  High quality sequence start: 14
  High quality sequence stop: 337.
  Location/Qualifiers
    1..531
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone_lib="ST0284"
    /dev_stage="Adult"
    /note="Organ: stomach; Vector: puc18; Site_1: SmaI;
    Site_2: SmaI; A mini-library was made by cloning products
    derived from ORESTES PCR (U.S. Letters Patent application
    No. 196,716 - Ludwig Institute for Cancer Research)
    profiles into the puc 18 vector. Reverse transcription of
    tissue mRNA and cDNA amplification were performed under
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	low stringency conditions."
BASE COUNT	103 a 149 c 169 g 110 t
ORIGIN	

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alignment_scores:
  quality: 625.00
  ratio: 5.040
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  percent_identity: 96.094
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alignment_block:
US-09-786-130-1 x AW393201/rev ..
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Align seg 1/1 to reverse of: AW393201 from: 1 to: 531

38	GIuValhTrpProgluValGluValProleuasnnglyTrpLeuSerle	54
530	GAAGTACCAGCGGCAMAGAGTGGAACTGCCACCTGAATGGAAACGCTGACCTT	481
54	uSerCysValAlaCysSerArgPheProAsnPheserTrileuylTrpL	71
480	ATCCTGTGTGGCGCTGGAGCGGCTTCCCAACTGACATCCTCTACAGGC	431
71	euclyasnclysSerPheIleGluHisLeuProGlyArgLeuTrp.GluI	87
430	TGGCGAATGATTCCTTCATTTAGACACCTCCAGAGCGCATGTGGGAGGG	381
87	ySerTrlSerArgGluArgGlySerThrGlyThrGluLeucysArgLal	104
380	GAGCACCAGCCGGAGAACGTGGAGACACAGTACGAGCTTTTTCAGAGCCT	331
104	euValLeuGluGlnLeuThrProAlaLeuHisSerThrAsnPheSerCys	120
330	TGGTGTGTGAGACAGCTGACACCTGCCCTGCACAGACCAACTTCTCCTGT	281
121	ValLeuValAspProGluGlnValValGlnArgHisValValLeuAlaGly	137
280	GTCCTGTGTGACCCCTGAACAGGTTTCCAGAGGTACAGCTGCTGGGCCCA	231
137	nleuTrpAlaGlyLeuArgAlaThrLeuProProThrGlnGluAlaLeuP	154
230	GCCTGGGCGGGGTGAGGCACTTCCGCCCAACCAAGAACCTCTGC	181
154	roSerSerHisSerSerProGlnGlnGlnGly	164
180	CCTCCAGCCACACAGAGTCCACAGCGACGAGGCT	149

seq.documentation_block: 515 bp mRNA linear EST 24-NOV-2000
LOCUS BF375685
DEFINITION RC5:CTG300-151299-031-E04 ST0300 Homo sapiens CDNA, mRNA sequence.
ACCESSION BF375683
VERSION BF375685.1 GI:11337710
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202663
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL:
<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC5&t2=RC5-ST0300-151299-031-E04&t3=1999-12-15&t4=1>
Seq primer: puc 18 forward
High quality sequence start: 44
High quality sequence stop: 60.

FEATURES

Source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="ST0300"
/dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site:1: Sma1;
Site:2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196, 716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT      105 a      163 c      149 g      98 t
ORIGIN

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alignment_scores:
  Quality: 622.00
  Ratio: 4.937
  Percent Similarity: 94.737
  Length: 133
  Gaps: 1
  Percent Identity: 92.481
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alignment_block:

Align seg 1/1 to: BF375685 from: 1 to: 515

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33  GlnCysProAlaLeuAlaThrThrProGluValAlaProLeuAs 49
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2  GAGAGTCACACATGGAAATGACCTGGCCAGAGAGAAAGGCCATGA 51
   ...: ||||| ||||| ||||| ||||| ||||| ||||| |||||
49  ncjYhrLeuSerLeu.SerCysValAlaCysSerArgPheProAspPhe 65
   ...: ||||| ||||| ||||| ||||| ||||| ||||| |||||
52  TGGAGCGCTCAGCGGTGTCGGGTGAGGCGCTGACGCCGCTCCCAACTTC 101
   ...: ||||| ||||| ||||| ||||| ||||| ||||| |||||
66  SerIleLeuTyrTrpLeuAluSncIysSerPheIleGluHisLeuProG1 82
   ...: ||||| ||||| ||||| ||||| ||||| ||||| |||||
102  AGATATCTCTACAGGTGGGGCAATGTTCCTTCATATGACATCCCAAG 151
   ...: ||||| ||||| ||||| ||||| ||||| ||||| |||||
82  yArgLeuTrpGluGlySerThrSerArgGluArgGlySerThrGlyThrG 99
   ...: ||||| ||||| ||||| ||||| ||||| ||||| |||||
152  CGCAGCTGGGAGAGGGAGCACCAGCCGCTTAACGTGGAGCAGACAGTACG 201
   ...: ||||| ||||| ||||| ||||| ||||| ||||| |||||
99  LncCysLysAlaLeuValLeuGluGluInLeuThrProAlaLeuHisSer 115
   ...: ||||| ||||| ||||| ||||| ||||| ||||| |||||
202  AGCTGTGCAGAGGCTGTGTGTGTGGAGCAGCTGACCCCTGGCCCTCACAGC 251
   ...: ||||| ||||| ||||| ||||| ||||| ||||| |||||
116  ThrAspPheSerCysValAlaLeuValAspProGluGlnValValGlnAspG1 132
   ...: ||||| ||||| ||||| ||||| ||||| ||||| |||||
252  ACCAACTTTTCTGTGTGTCTGTGGACCCCTGACACAGGTTGTCCAGCGTCA 301
   ...: ||||| ||||| ||||| ||||| ||||| ||||| |||||
132  sValValLeuAlaGluInLeuTrpAlaGlyLeuAlaArgAlaThrLeuProProT 149
   ...: ||||| ||||| ||||| ||||| ||||| ||||| |||||
302  CGTCTGTCTGGCCCAACACTGTGGGCTGAGGCGTGAAGGCCAACCTTGGCCCCCA 351
   ...: ||||| ||||| ||||| ||||| ||||| ||||| |||||
149  hrcInGluAlaLeuProSerSerHisSerSerProGlnGlnGlnGly 164
   ...: ||||| ||||| ||||| ||||| ||||| ||||| |||||
352  CCCAAGAGAACCCCTGGCCCTTCACACCCACAGTCCACAGCACAGGAGGT 398
   ...: ||||| ||||| ||||| ||||| ||||| ||||| |||||

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seq_documentation_block:
LOCUS      B1822872                901 bp    mRNA    linear    EST 04-OCT-2001
DEFINITION 603040310F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5181242 5',
            mRNA sequence.
ACCESSION  B1822872
VERSION    B1822872.1 GI:15934422
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE  1 (bases 1 to 901)
AUTHORS   NIH-MGC http://mgs.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Email: cgapbs-remail.nih.gov
            Contact: Robert Strausberg, Ph.D.
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LHAM11452 row: c column: 03
            High quality sequence stop: 856.
            Location/Qualifiers
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                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone_image="5181242"
                /clone_lib="NIH_MGC_115"
                /lab_host="DH10B"
                /note="Organ: pooled brain, lung, testis; Vector:
                pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                source anonymous pool of 6 male brains, age range 23-27; 1
                male lung, age 27; and 1 male testis, age 69. Library is
                oligo-dT primed and directionally cloned (EcoRV site is
                destroyed upon cloning). Average insert size 1.8 kb,
                insert size range 1-3 kb. Library is normalized and
                enriched for full-length clones and was constructed by C.
                Gruber (Invitrogen). Research Genetics tracking code
                021. Note: This is a NIH-MGC Library."

BASE COUNT  188 a      276 c      245 g      192 t
ORIGIN
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            Ratio: 4.252      Gaps: 7
            Percent Similarity: 89.809      Percent Identity: 83.439

alignment_block:
US-09-786-130-1 x B1822872 ..
Align seg 1/1 to: B1822872 from: 1 to: 901

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83  rgleutrpglu.glyserthrserarggluargglyserthrglthr 99
|||||
683  gactgtggcacgggagaccagccgagaccgtggacacagctaccsca 732
99  pleucyslysalaleuvalleugluglnleuthrproalaenisert 116
|||||
733  gcgtggcaagccttgctgctggagcagctgacccctggcctccagcca 782
116  hrasnphesercys.valleuvalaspproglnvalvalargh 132
783  ccaattctctcctgtgctgtgctggaccttgaaacaggtggccagctcc 832
132  sva1valleuvalaglnleu...trpalaglyleuargalatrleuprop 148
833  cgtcgtcctggccagctgctggctggct.....gagggaccttgcccc 876
148  rothrnglnlu 151
||
877  caccacaggaag 887

seq_name: gb_est1:AW393194
seq_documentation_block:
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DEFINITION CM2-ST0284-061299-046-d12 ST0284 Homo sapiens cDNA, mRNA sequence.
ACCESSION  AW393194
VERSION    AW393194.1 GI:6897853
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE  1 (bases 1 to 538)
AUTHORS   HCGP http://www.ludwig.org.br/ORESTES.
TITLE     The FAPESP/LICR Human Cancer Genome Project
JOURNAL   Unpublished (1999)
COMMENT   Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar. 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?tl-CM2at2-CM2-ST0284-
            061299-046-d12at3=1999-12-06&tl=1)
            Seq primer: puc 18 forward
            High quality sequence start: 13
            High quality sequence stop: 500.
            Location/Qualifiers
                1..538
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone_lib="ST0284"
                /dev_stage="Adult"
                /note="Organ: stomach; Vector: puc18; Site_1: SmaI;
                Site_2: SmaI; A mini-library was made by cloning products
                derived from ORESTES PCR (U.S. Letters Patent application
                No. 196,716 - Ludwig Institute for Cancer Research)
                profiles into the puc 18 vector. Reverse transcription of
                tissue mRNA and cDNA amplification were performed under
                low stringency conditions."

BASE COUNT  104 a      152 c      174 g      108 t
ORIGIN
alignment_scores:

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Quality: 594.00 Length: 133
Ratio: 4.677 Gaps: 6
Percent Similarity: 95.489 Percent Identity: 94.737

alignment_block:

us-09-786-130-1 x AW393194/rev ..

Align seg 1/1 to reverse of: AW393194 from: 1 to: 538

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38 GluVal1hrTPrProGluVal1GluVal1ProLeuAsnGlyThrLeuSerLe 54
|||||
531 GAAGTGACCTGGCCAGATGGAGTGCCACTGAATGGAAGCTGAGACTT 482
|||||
54 user.CysValAlaCysSerArgPheProasn.PheSerIleLeuTyTr 70
|||||
481 ATCCTTGtGtGCGCTGCAGCGGCTTCCCAACTTTCAGCATCTCTACTG 432
|||||
70 pLeuGlyAsnGlySerPheIle.GluHisLeu.ProGlyArgLeuTrpG1 86
|||||
431 GCTGGCAATGTTCTTCATTGAGCACCTCCCGAGCGGACTGTGGGA 382
|||||
86 uGlySerThrSerArg.GluArgGlySerThrGlyThrGln.LeuCysLy 102
|||||
381 GGGGAGCACCGCGGGGAACGTGGGAGCACAGGTACGACACTTGTGCAA 332
|||||
102 sAlaLeuValLeuGluGlnLeuThrProAlaLeuHisSerThrAsnPhes 119
|||||
331 GGCCTTGtGtGCTGAGCAGCTGACCCCTGCCCTGCACAGCACCACTTCT 282
|||||
119 erCysValLeuValAspProGluGlnValAlaGlnArgHisValLeu 135
|||||
281 CCTGTGTGCTGCTGAGACCTGAACAGGTGTGCCAGCGTCAAGTGTCTG 232
|||||
136 AlagIleuThrPrAlaGlyLeuArgAlaThrLeuProThrGlnGluAl 152
|||||
231 GCCAGCTCTGGGCTGGGCTGAGGGCAACCTTGCCCCCAGCCCAAGAAGC 182
|||||
152 aLeuProSerSerHisSerSerProGlnGlnGly 164
|||||
181 CTTGCCCTCCAGCCAGCAGATCCACAGCAGCAGAGGT 145
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 22:51:49 ; Search time 66.54 Seconds
(without alignments)
426.378 Million cell updates/sec

Title: US-09-786-130-1

Perfect score: 870

Sequence: 1 TPVSQTTTAAATASVRSSTKDP.....TLPPQALPSSHSPPQOQG 164

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL_19:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mhcc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	870	100.0	184	4	Q9UNH2	Q9unh2 homo sapien
2	870	100.0	194	4	Q9UBR7	Q9ubr7 homo sapien
3	525	60.3	161	4	Q9NZA9	Q9nza9 homo sapien
4	523.5	60.2	153	11	Q9JUN2	Q9jin2 ratius norv
5	523	60.1	191	11	Q9ZOM9	Q9zom9 mus musculu
6	515	54.9	193	11	Q9QUH2	Q9quh2 mus musculu
7	477.5	54.9	192	11	Q9ZON0	Q9zoh0 mus musculu
8	302.5	34.8	99	11	Q9CY30	Q9cy30 mus musculu
9	217	24.9	218	12	Q9TMI3	Q9tmi3 molluscum c
10	205	23.6	235	12	Q98Z22	Q98z22 molluscum c
11	164	18.9	133	12	Q98Z21	Q98z21 molluscum c
12	124	14.3	161	12	Q910Q1	Q910q1 lumby skin
13	115.5	13.3	136	12	Q9DHU8	Q9dhu8 yaba-like d
14	104.5	12.0	120	12	O57169	O57169 vaccinia vi
15	98.5	11.3	124	12	P87608	P87608 cowpox viru
16	96.5	11.1	658	4	Q9NZN0	Q9nzn0 homo sapien

17	96.5	11.1	686	4	Q9NP60	Q9np60 homo sapien
18	95.5	11.0	126	12	Q9IC13	Q9ic13 vaccinia vi
19	95.5	11.0	126	12	Q9IWI2	Q9iwi2 ectromella
20	94.5	10.9	126	12	Q07044	Q07044 variola vir
21	93.5	10.7	126	12	Q85357	Q85357 variola vir
22	93.5	10.7	126	12	Q89067	Q89067 variola vir
23	93	10.7	1034	5	Q9TXP2	Q9txp2 caenorhabdi
24	92.5	10.6	138	12	Q85319	Q85319 ectromella
25	92.5	10.6	354	11	Q9ER66	Q9er66 mus musculu
26	92.5	10.6	686	11	Q9ERS6	Q9ers6 mus musculu
27	84.5	9.7	286	10	Q9W022	Q9w022 aradidopsis
28	84.5	9.7	291	10	Q9ZS87	Q9zs87 aradidopsis
29	84.5	9.7	341	10	Q93YW7	Q93yw7 aradidopsis
30	82.5	9.5	418	11	Q70426	Q70426 ratius norv
31	82.5	9.5	1241	4	Q60500	Q60500 homo sapien
32	82.5	9.5	2043	5	Q96943	Q96943 geodia cydo
33	82	9.4	794	2	P72249	P72249 rhodobacter
34	81	9.3	627	5	Q9XW47	Q9xw47 rhodobacter
35	81	9.3	1478	11	Q88923	Q88923 ratius norv
36	81	9.3	1487	11	Q92174	Q92174 ratius norv
37	81	9.3	1616	4	Q15054	Q15054 homo sapien
38	80	9.2	359	5	Q26596	Q26596 schistosoma
39	80	9.2	674	4	Q9NV06	Q9nv06 homo sapien
40	79	9.1	547	6	Q9G465	Q9g465 brassica ju
41	79	9.1	313	8	Q9BGV2	Q9bgv2 macaca fasc
42	79	9.1	628	10	Q9XIC7	Q9xic7 aradidopsis
43	79	9.1	628	10	Q9AF63	Q9af63 aradidopsis
44	79	9.1	643	4	Q9NSC0	Q9nsg0 homo sapien
45	79	9.1	674	4	Q75807	Q75807 homo sapien

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	184 AA.
Q9UNH2	Q9UNH2			
AC	Q9UNH2			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	MC51L-53L-54L HOMOLOG (FRAGMENT).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99263157; PubMed=10329540;			
RA	Xiang Y., Moss B.;			
RT	"Identification of human and mouse homologs of the MC51L-53L-54L			
RT	family of secreted glycoproteins encoded by the Molluscum contagiosum			
RT	poxvirus.";			
RL	Virology 257:297-302(1999).			
DR	EMBL: AF122908; AAD41053.1; -			
DR	InterPro: IPR003006; Ig_MHC.			
DR	Pfam: PF00047; Ig, 1.			
FT	NON_TER			
SO	SEQUENCE	184 AA;	19629 MW;	FABI2D64BA6FD3A2 CRC64;

Query Match Best Local Similarity 100.0%; Score 870; DB 4; Length 184; Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TPVSQTTTAAATASVRSSTKDPSPVPVPAKQCPALEVTWPEVEVPLNGTSLSCVACS	60
DB	21	TPVSQTTTAAATASVRSSTKDPSPVPVPAKQCPALEVTWPEVEVPLNGTSLSCVACS	80
QY	61	REPNSITLWNGSFTLHPLGRMEGSTSRSGSTGQLCKALVLEDTTALHSTNSC	120
DB	81	REPNSITLWNGSFTLHPLGRMEGSTSRSGSTGQLCKALVLEDTTALHSTNSC	140

```

QY 121 VLVDPEQVYVQRHVLAQLMAGLRATLPPTQELPSSHSPQOOG 164
DB 141 VLVDPEQVYVQRHVLAQLMAGLRATLPPTQELPSSHSPQOOG 184

RESULT 2
Q9UBR7 PRELIMINARY: PRT; 194 AA.
ID Q9UBR7
AC Q9UBR7
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DR 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE INTERLEUKIN-18 BINDING PROTEIN PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=99192308; PubMed=10094485;
RA Aizawa Y., Akita K., Tanai M., Korigoe K., Mori T., Nishida Y.,
RA Ushio S., Nukada Y., Tanimoto T., Ikegami H., Ikeda M., Kurimoto M.,
RT "Cloning and expression of interleukin-18 binding protein.";
RL FEBS Lett. 445:338-342(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99263157; PubMed=10329540;
RA Xiang Y., Moss B.;
RT "Identification of human and mouse homologs of the MCS1L-53L-54L
RT family of secreted glycoproteins encoded by the MolLusum contagiosum
RT poxvirus.";
RL Virology 257:297-302(1999).
DR EMBL; AB019504; BAA76374.1; -
DR EMBL; AF122906; AAD41051.1; -
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig_1.
KW Signal.
FT SIGNAL. 1 30 POTENTIAL.
FT CHAIN 31 194 INTERLEUKIN-18 BINDING PROTEIN.
SQ SEQUENCE 194 AA; 21099 MW; 5E520D646AFA843 CRC64;

Query Match 100.0%; Score 870; DB 4; Length 194;
Best Local Similarity 100.0%; Pred. No. 5e-83;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPVSQTTAATASVSTKDCPSOPVPFPAKQCPALVETWPEVEVPLNGTSLSCVACS 60
DB 31 TPVSQTTAATASVSTKDCPSOPVPFPAKQCPALVETWPEVEVPLNGTSLSCVACS 90
QY 61 RPPNFSILYWLNGSGFIEHLPGRLWEGSTSRERGSTGTOLCKALVLEQLTPALHSTNFSC 120
DB 91 RPPNFSILYWLNGSGFIEHLPGRLWEGSTSRERGSTGTOLCKALVLEQLTPALHSTNFSC 150
QY 121 VLVDPEQVYVQRHVLAQLMAGLRATLPPTQELPSSHSPQOOG 164
DB 151 VLVDPEQVYVQRHVLAQLMAGLRATLPPTQELPSSHSPQOOG 194

RESULT 3
Q9NZA9 PRELIMINARY: PRT; 161 AA.
ID Q9NZA9
AC Q9NZA9
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DR 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, last annotation update)
DE INTERLEUKIN-18 BINDING PROTEIN D.
GN IL18BP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20122593; PubMed=10655506;
RA Kim S.H., Eisenstein M., Reznikov L., Fantuzzi G., Novick D.,
RA Rubinstein M., Dinarello C.A.;
RT "Structural requirements of six naturally occurring isoforms of the
RT IL-18 binding protein to inhibit IL-18.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1190-1195(2000).
DR EMBL; AF215907; AAF31697.1; -
SQ SEQUENCE 161 AA; 17246 MW; 28A04CCD92F4833D CRC64;

Query Match 60.3%; Score 525; DB 4; Length 161;
Best Local Similarity 100.0%; Pred. No. 4.1e-47;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPVSQTTAATASVSTKDCPSOPVPFPAKQCPALVETWPEVEVPLNGTSLSCVACS 60
DB 29 TPVSQTTAATASVSTKDCPSOPVPFPAKQCPALVETWPEVEVPLNGTSLSCVACS 88
QY 61 RPPNFSILYWLNGSGFIEHLPGRLWEGSTSRERGSTG 97
DB 89 RPPNFSILYWLNGSGFIEHLPGRLWEGSTSRERGSTG 125

RESULT 4
Q9JLN2 PRELIMINARY: PRT; 193 AA.
ID Q9JLN2
AC Q9JLN2
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DR 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, last annotation update)
DE INTERLEUKIN 18 BINDING PROTEIN.
GN IL18BP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LEWIS;
RA Im S.H., Venkatesh N., Barchan D., Souroujon M.C., Fuchs S.;
RT "Cloning and characterization of rat IL-18 binding protein.";
RL Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF154569; AAF72102.1; -
SQ SEQUENCE 193 AA; 21085 MW; BDB23D80E44B4B0 CRC64;

Query Match 60.2%; Score 523.5; DB 11; Length 193;
Best Local Similarity 64.0%; Pred. No. 7.4e-47;
Matches 103; Conservative 14; Mismatches 43; Indels 1; Gaps 1;

QY 4 SQTTAATASVSTKDCPSOPVPFPAKQCPALVETWPEVEVPLNGTSLSCVACSRRP 63
DB 30 SAPLTATVLTTRSSKDCPSQSPVPAKQCPALVETWPEVEVPLNGTSLCTACSRPP 88
QY 64 NFSILYWLNGSGFIEHLPGRLWEGSTSRERGSTGTOLCKALVLEQLTPALHSTNFSCVLY 123
DB 89 NFSILYWLNGSGFIEHLPGRLWEGSTSRERGSTGTOLCKALVLEQLTPALHSTNFSCVLY 148
QY 124 DPEQVYVQRHVLAQLMAGLRATLPPTQELPSSHSPQOOG 164
DB 149 DPEQVYVQRHVLAQLMAGLRATLPPTQELPSSHSPQOOG 189

RESULT 5
Q9ZOM9 PRELIMINARY: PRT; 191 AA.
ID Q9ZOM9
AC Q9ZOM9
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DR 01-MAY-1999 (TREMBLrel. 10, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE INTERLEUKIN-18 BINDING PROTEIN D PRECURSOR.

```

... (5) SENTENCE FROM N A
RP

RT "Interleukin-18 binding protein: a

Классификация "А"

Query Match	54.9%	Score 477.5	DB 11	Length 192
Best Local Similarity	68.3%	Pred. No. 4.6e-42		
Matches 95	Conservative 10	Mismatches 31	Indels 3	Gaps 2

RESULT	8
Q9CV30	
ID	Q9CV30
PRELIMINARY;	
PRT;	99 AA

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE,

RX MEDLINE-21085660; PubMed-11217851;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa Y., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 RA Kodota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., Ring B., Kochaya H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudli F., Suzuki R., Tomlita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baladrelli R., Barsh G.,
 RA Blake J., Boiffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gutschind S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitteker C., Wilming L.,
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.",
 RL Nature 409:685-690(2001).
 DR EMBL; AK009877; BAB26558.1; -.
 FT MGD; MGI:1333800; Igfbp.
 SQ NON_TER 1
 99 AA; 10869 MW; 2CB08739D5AAB8BC CRC64;

Query Match	34.88;	Score 302.5;	DB 11;	Length 99;
Best Local Similarity	67.48;	Pred. No. 4e-24;		

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QY      70  WLGNGSFIEHLPGRAWEGSTSRERGSTGTQLCKALVEQLTPALHSTNESCVLVE
          |||||  |||||  |||||  :|||  :|||  :|||  :|||  :|||  :|||
Db      1  WLGNGSFIEHLPGRAKEGHTSRERHNTSTWLHRAIVEELSPTLRSTNESCFLVD

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RESULT	9	
Q9IW13		
ID	Q9IW13	PRELIMINARY;
		PRT;
		218 AA

Query Match Similarity	24.9%	Score 217;	DB 12;	Length 218;
Best Local Similarity	39.9%	Pred. No. 8.3e-15;		
Matches 55; Conservative	24;	Mismatches 45;	Indels 14;	Gaps 6

RESULT	10	
ID	Q98222	PRELIMINARY;
	Q98222	PRT;
	Q98222	235 AA.

DT	01-FEB-1997	(TREMBLrel. 02, Created)
DT	01-FEB-1997	(TREMBLrel. 02, Last sequence update)
DT	01-NOV-1998	(TREMBLrel. 08, Last annotation update)
DE	MC054L.	
GN	MC054L.	
OS	Molluscum contagiosum virus subtype 1 (MCV1).	
OC	viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae.	
OC	Molluscipoxvirus.	
OX	NCBI_TaxID=10280;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=96325459; PubMed=8670425;	
RA	Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G.,	
RA	Moss B.;	
RT	"Genome sequence of a human tumorigenic poxvirus: Prediction of	
RT	specific host response-evasion genes.";	

ID	Q91001	PRELIMINARY;	PRT;	161	AA.
AC	091001				

LEE H. C. ;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 19, 2002, 21:48:54 ; Search time 57.81 Seconds
(without alignments)
315.103 Million cell updates/sec

Title: US-09-786-130-1
Perfect score: 870
Sequence: 1 TPVSGTTTAATATVSRFTKDP.....TLPPTEALPSSHSPPQOG 164

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
A.Geneseq_032802:*
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21: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	870	100.0	164	21	AAV83951 Human mature inter-
2	870	100.0	192	20	AAW98004 Human interleukin-
3	870	100.0	194	21	AAV96292 Human IGFAW-4 immu
4	870	100.0	194	21	AAV83985 Full length human
5	742	85.3	197	20	AAW98006 Human interleukin-
6	727	83.6	137	21	AAV83982 Human IL-18 bindin
7	525	60.3	161	20	AAW98007 Human interleukin-
8	515	59.2	165	21	AAV83952 Mouse mature inter
9	515	59.2	193	21	AAV83989 Full length mouse
10	441	50.7	117	21	AAV83986 Mouse IL-18 bindin
11	257	29.5	113	20	AAW98005 Human interleukin-

12	244	28.0	47	21	AAV83964 Human IL-18 bindin
13	209	24.0	40	20	AAW98008 Human interleukin-
14	122	14.0	55	20	AAV12716 Human 5' EST sece
15	114	13.1	29	21	AAV83960 Human interleukin
16	114	13.1	55	20	AAV12556 Human 5' EST sece
17	106	12.2	134	18	AAW26423 Swinepox virus H1n
18	106	12.2	14	22	AAW68244 Protein encoded by
19	102.5	11.8	45	21	AAV83968 Mouse IL-18 bindin
20	101	11.6	23	21	AAV83958 Human interleukin
21	96.5	11.1	59	20	AAV14130 Human IL-18D8 prot
22	96.5	11.1	658	20	AAV22164 Human TIGIR prote
23	96.5	11.1	666	20	AAV14128 Human IL-18D8 prot
24	93.5	10.7	2134	22	AAV27624 Novel human diagno
25	92.5	10.6	385	22	ABG02770 Novel human diagno
26	92.5	10.6	532	22	ABG20407 Novel human diagno
27	92.5	10.6	717	22	ABG24052 Novel human diagno
28	92.5	10.6	744	22	ABG02772 Novel human diagno
29	90	10.3	49	21	AAV83983 Human IL-18 bindin
30	88.5	10.2	766	22	ABG14630 Novel human diagno
31	87.5	10.1	949	22	ABG06446 Novel human diagno
32	84.5	9.7	341	21	AAV41565 Arabidopsis thalia
33	82.5	9.5	1241	20	AAV42167 Human nephrit prol
34	82.5	9.5	1241	22	AAV47047 Human nephrit. Ho
35	81	9.3	430	22	ABG14501 Novel human diagno
36	81	9.3	945	20	AAV06119 Human CIITA intera
37	80	9.2	22	21	AAV83953 Human interleukin
38	80	9.2	674	22	AAV82888 Human protein sequ
39	80	9.2	1072	22	ABG04157 Novel human diagno
40	79.5	9.1	307	22	AAV40911 Propionibacterium
41	79	9.1	237	20	AAV6187 Human bladder tumo
42	79	9.1	467	21	AAV30869 Arabidopsis thalia
43	79	9.1	598	21	AAV30868 Arabidopsis thalia
44	79	9.1	628	21	AAV30867 Arabidopsis thalia
45	79	9.1	674	20	AAV99891 Human growth regul

ALIGNMENTS

RESULT 1
AAV83951 standard; Protein; 164 AA.
XX
XX AAV83951;
AC
XX
DT 28-JUL-2000 (first entry)
XX
DE Human mature Interleukin 18 binding protein.
XX
KW Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
KW regulator; drug; sensitivity disease; organ rejection; organ transplant;
KW autoimmune disease.
XX
XX Homo sapiens.
XX
PN WO200012555-A1.
XX
PD 09-MAR-2000.
XX
PF 18-NOV-1998; 98WO-0P05186.
XX
PR 01-SEP-1998; 98JP-0247588.
PR 18-NOV-1998; 98JP-0327914.
(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PI Torioge K, Tanial M, Kurimoto M;
DR WPI: 2000-237850/20.
DR N-PSDB; AAA11002.
XX
XX Interleukin 18-binding protein with activity of regulating
PT physiological actions of interleukin 18, useful as regulator and drug

PT for sensitivity diseases and organ rejection and in treating diseases
PT due to excess immune reaction -
PS Claim 1; Page 44-45; 71pp; Japanese.
XX
CC The invention relates to novel interleukin 18 (IL-18)-binding proteins
CC from humans or mice which act as regulators and drugs for sensitivity
CC diseases and organ rejection and in treating diseases due to excess
CC immune reaction, e.g. in slowing down rejection after organ transplant,
CC and in treating autoimmune diseases. This sequence represents the mature
CC human interleukin 12 binding protein.
XX
SQ Sequence 164 AA:

Query Match 100.0%; Score 870; DB 21; Length 164;
Best Local Similarity 100.0%; Pred. No. 1.2e-78;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPVSQTTTAATASVSTKDCPSQPPVFPAAKQCPALVETWPEVPLNGTSLSCVACS 60
DB 1 TPVSQTTAATASVSTKDCPSQPPVFPAAKQCPALVETWPEVPLNGTSLSCVACS 60
QY 61 RPPNFSIIYWGNGSFIEHLPGRLEWEGSTRSGSTGTOLCKALVLEDTPALHSTNFS 120
DB 61 RPPNFSIIYWGNGSFIEHLPGRLEWEGSTRSGSTGTOLCKALVLEDTPALHSTNFS 120
QY 121 VLVDPEQVYVORHVVLAQLMAGLRATLPPTQEALPSSHSSPQOQG 164
DB 121 VLVDPEQVYVORHVVLAQLMAGLRATLPPTQEALPSSHSSPQOQG 164
DB 121 VLVDPEQVYVGRHVLAQLMAGLRATLPPTQEALPSSHSSPQOQG 164

RESULT 2
AAW98004
ID AAW98004 standard; Protein: 192 AA.
XX
AC AAW98004;
XX
DT 21-JUN-1999 (first entry)
XX
DE Human interleukin-18 binding protein splice variant IL-18Bpa.
XX
KW Interleukin-18 binding protein; IL-18BP; IL-18Bpa; splice variant;
KW human; autoimmune disease; inflammation; diabetes; pancreatitis;
KW rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis;
KW psoriasis; inflammatory bowel disease; multiple sclerosis;
KW ischemic heart disease; ischemic brain injury; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..28
FT /note="signal peptide"
FT Protein 29..192
FT /note="mature protein"
XX
PN WO9909063-A1.
XX
PD 25-FEB-1999.
XX
PE 13-AUG-1998; 98WO-IL00379.
XX
PR 22-JUL-1998; 98IL-0125463.
PR 14-AUG-1997; 97IL-0121554.
PR 27-AUG-1997; 97IL-0121639.
PR 29-SEP-1997; 97IL-0121860.
PR 06-NOV-1997; 97IL-0122134.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Dinarello C, Kim SH, Novick D, Rubinstein M;
XX
DR WPI; 1999-180975/15.

DR N-PSDB: AAX24749.
XX
XX New interleukin-18 binding protein - useful for treating human
PT diseases, including autoimmune disease and inflammation
XX
PS Claim 3; Page 53-54; 100pp; English.
XX
XX The present sequence represents a human interleukin-18 binding
CC protein (IL-18BP) splice variant designated IL-18Bpa. This
CC is one of 4 novel splice variants (see also AAW98005-07); all
CC putative soluble proteins, encoded by cDNA clones (see AAX24749-52)
CC detected following a screening of human peripheral blood monocyte,
CC Jurkat T-cell, peripheral blood mononuclear cell and spleen cell
CC cDNA libraries. IL-18Bpa is the most abundant of the 4 splice
CC variants and is a putative member of the immunoglobulin superfamily.
CC Its first 40 residues perfectly match the N-terminal sequence of
CC urinary IL-18BP (see AAW98008). IL-18BP polypeptides capable of
CC binding IL-18 and/or modulating and/or blocking IL-18 activity are
CC provided. Methods for their isolation and recombinant production,
CC DNA vectors expressing them, vectors useful for their expression in
CC humans and other mammals, and antibodies against them are also
CC provided. IL-18BP polypeptides, and DNA encoding them, can be used
CC to treat conditions requiring the protein (claimed). Conditions
CC include autoimmune diseases, type I diabetes, rheumatoid arthritis,
CC graft rejections, inflammatory bowel disease, sepsis, multiple
CC sclerosis, ischemic heart diseases, ischemic brain injury, chronic
CC hepatitis, psoriasis, and chronic/acute pancreatitis. IL-18BP is
CC also useful for purifying IL-18 (claimed).
XX
SQ Sequence 192 AA:

Query Match 100.0%; Score 870; DB 20; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.5e-78;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPVSQTTTAATASVSTKDCPSQPPVFPAAKQCPALVETWPEVPLNGTSLSCVACS 60
DB 29 TPVSQTTAATASVSTKDCPSQPPVFPAAKQCPALVETWPEVPLNGTSLSCVACS 88
QY 61 RPPNFSIIYWGNGSFIEHLPGRLEWEGSTRSGSTGTOLCKALVLEDTPALHSTNFS 120
DB 89 RPPNFSIIYWGNGSFIEHLPGRLEWEGSTRSGSTGTOLCKALVLEDTPALHSTNFS 148
QY 121 VLVDPEQVYVORHVVLAQLMAGLRATLPPTQEALPSSHSSPQOQG 164
DB 121 VLVDPEQVYVGRHVLAQLMAGLRATLPPTQEALPSSHSSPQOQG 192

RESULT 3
AAW96292
ID AAW96292 standard; protein: 194 AA.
XX
AC AAW96292;
XX
DT 16-AUG-2000 (first entry)
XX
DE Human IGFAM-4 immunoglobulin.
XX
KW Human; immunoglobulin; IGFAM-4; IGFAM; immune disorder; cancer;
KW infection; inflammation; haematopoiesis; AIDS; allergy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT /label= signal_peptide
FT Protein 31..194
FT /label= IGFAM-4
XX
PN WO200029583-A2.
XX
PD 25-MAY-2000.


```

XX 19-NOV-1999; 99WO-US27566.
PF
XX 19-NOV-1998; 99US-0113635.
PR 22-DEC-1998; 98US-0113635.
PR 07-APR-1999; 99US-0128194.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR,
PI Lu DAM, Lai P, Hillman JL, Yang J;
XX
DR WPI; 2000-387796/33.
DR N-PSDB; AAA27384.
XX
PT Immunoglobulin superfamily proteins, the agonist and antagonist of the
PT protein is useful for preventing and treating disorders associated with
PT altered levels of the protein such as cancer, immune system disorders
PT
XX
PS Claim 1; Page 81; 105pp; English.
XX
CC The present sequence is the human immunoglobulin superfamily protein
CC IGFAM-4. Its gene was isolated from a cDNA library of prostate tumour
CC tissue. It is expressed in nervous, haematopoietic and immune and
CC cardiovascular tissue, where cancer and inflammation are common. The
CC gene, protein, its antibodies, agonists and antagonists are suitable for
CC diagnosing and treating many diseases, including cancer, immune system
CC disorders (such as inflammation, AIDS, allergies, anaemia,
CC arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's
CC disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,
CC multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,
CC systemic lupus erythematosus and ulcerative colitis), complications of
CC cancer, haemodialysis and extracorporeal circulation, trauma and
CC haematopoietic cancer (such as leukaemia) and infections caused by
CC bacteria, viruses, fungi or parasites.
XX
SQ Sequence 194 AA;

```

```

Query Match 100.0%; Score 870; DB 21; Length 194;
Best Local Similarity 100.0%; Pred. No. 1.5e-78;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 TPVSQTTTAATASVRSRKDCPSOPVFPAAKOCPALEVTWPEVEVPLNGTSLSCVACS 60
DB 31 tpvsqtttaataasvrsrkdcpsqpvfpaaqgcpalavtwpevevplngtislscvacs 90
QY 61 RFPNFSILYWLGNCSFTEHLPGRLMEGSTSRERGSTGTQLCKALVLEBOLTPALHSTNFS 120
DB 91 rfpnfsillywlgnsgfiehlpgrlwegstsrergstgtqlckalvleqlpalhstnfsc 150
QY 121 VLVDPQGVQORHVYLAOLMAGLRATLPPTQALPSSSHSSPOQOG 164
DB 151 vlvdpqgvqgrhvvlaqlwaglratlptqalpsshspqgqg 194

```

```

RESULT 4
AAW83985
ID AAW83985 standard; Protein; 194 AA.
AC
XX
AC AAW83985;
XX
DT 28-JUL-2000 (first entry)
XX
DE Full length human interleukin 18 binding protein.
XX
KW Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
KW regulator; drug; sensitivity disease; organ rejection; organ transplant;
KW autoimmune disease.
XX
OS Homo sapiens.
XX

```

```

FH Key Location/Qualifiers
FT Peptide 1..30
FT /label= signal_peptide
FT Protein 31..194
FT /label= "mature human IL-18 binding protein"
XX
PN WO200012555-A1.
XX
PD 09-MAR-2000.
XX
XX 18-NOV-1998; 98WO-JP05186.
XX
PF 01-SEP-1998; 98JP-0247588.
PR 18-NOV-1998; 98JP-0327914.
XX
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Torigoe K, Tanai M, Kurimoto M;
XX
DR WPI; 2000-237850/20.
DR N-PSDB; AAA11007.
XX
XX
PT Interleukin 18-binding protein with activity of regulating
PT physiological actions of interleukin 18, useful as regulator and drug
PT for sensitivity diseases and organ rejection and in treating diseases
PT due to excess immune reaction
XX
PS Example 2; Page 63-64; 71pp; Japanese.
XX
CC The invention relates to novel interleukin 18 (IL-18)-binding proteins
CC from humans or mice which act as regulators and drugs for sensitivity
CC diseases and organ rejection and in treating diseases due to excess
CC immune reaction, e.g. in slowing down rejection after organ transplant,
CC and in treating autoimmune diseases. This sequence represents the full
CC length human interleukin 12 binding protein.
XX
SQ Sequence 194 AA;

```

```

Query Match 100.0%; Score 870; DB 21; Length 194;
Best Local Similarity 100.0%; Pred. No. 1.5e-78;
Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 TPVSQTTTAATASVRSRKDCPSOPVFPAAKOCPALEVTWPEVEVPLNGTSLSCVACS 60
DB 31 tpvsqtttaataasvrsrkdcpsqpvfpaaqgcpalavtwpevevplngtislscvacs 90
QY 61 RFPNFSILYWLGNCSFTEHLPGRLMEGSTSRERGSTGTQLCKALVLEBOLTPALHSTNFS 120
DB 91 rfpnfsillywlgnsgfiehlpgrlwegstsrergstgtqlckalvleqlpalhstnfsc 150
QY 121 VLVDPQGVQORHVYLAOLMAGLRATLPPTQALPSSSHSSPOQOG 164
DB 151 vlvdpqgvqgrhvvlaqlwaglratlptqalpsshspqgqg 194

```

```

RESULT 5
AAW98006
ID AAW98006 standard; Protein; 197 AA.
AC
XX
AC AAW98006;
XX
DT 21-JUN-1999 (first entry)
XX
DE Human interleukin-18 binding protein splice variant IL-18Bpc.
XX
KW Interleukin-18 binding protein; IL-18BP; IL-18Bpc; splice variant;
KW human; autoimmune disease; inflammation; diabetes; pancreatitis;
KW rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis;
KW psoriasis; inflammatory bowel disease; multiple sclerosis;
KW ischemic heart disease; ischemic brain injury; therapy.
XX
OS Homo sapiens.
XX

```

XX	Key	Location/Qualifiers
FH	Peptide	1..28
FT	Protein	/note= "signal peptide" 29..197
FT		/note= "mature protein"
XX		
PN	MO9909063-A1.	
XX		
PD	25-FEB-1999.	
XX		
PF	13-AUG-1998;	98WO-IL00379.
XX		
PR	22-JUL-1998;	98IL-0125463.
XX		
PR	14-AUG-1997;	97IL-0121554.
PR	27-AUG-1997;	97IL-0121639.
PR	29-SEP-1997;	97IL-0121860.
PR	06-NOV-1997;	97IL-0122134.
XX		
PA	(YEDA) YEDA RES & DEV CO LTD.	
XX		
PI	Dinareello C, Kim SH, Novick D, Rubinstein M;	
XX		
DR	WPI: 1999-180975/15.	
DR	N-PSDB: AAX24751.	
XX		
PT	New interleukin-18 binding protein - useful for treating human diseases, including autoimmune disease and inflammation	
XX		
PS	Claim 3; Page 58-59; 100pp: English.	
XX		
CC	The present sequence represents a human interleukin-18 binding protein (IL-18BP) splice variant designated IL-18BPc. This is one of four novel splice variants (see also AAW98004-07), all putative soluble proteins, that are encoded by cDNA clones (see AAX24749-52) detected following a screening of human peripheral blood monocyte, Jurkat T-cell, peripheral blood mononuclear cell and spleen cell cDNA libraries. IL-18BPc is a low abundance variant. IL-18BP polypeptides capable of binding IL-18 and/or modulating and/or blocking IL-18 activity are provided, as are methods for their isolation and recombinant production, DNA vectors expressing them, vectors useful for their expression in humans and other mammals, and antibodies against them. IL-18BP polypeptides, and DNA encoding them, can be used to treat conditions requiring the protein (claimed). Conditions include autoimmune diseases, type I diabetes, rheumatoid arthritis, graft rejections, inflammatory bowel disease, sepsis, multiple sclerosis, ischemic heart diseases, ischemic brain injury, chronic hepatitis, psoriasis, and chronic/acute pancreatitis. IL-18BP is also useful for purifying IL-18 (claimed).	
XX		
CC	Sequence 197 AA;	
SO		
Query Match	85.3%; Score 742; DB 20; Length 197;	
Best Local Similarity	100.0%; Pred. No. 8,2e-66;	
Matches 139; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 TPVSOQTAAATAVSRSTKDCPSQDPVPEPAKQCPALEVTWPEVNPINGTSLSCVACS 60	
Db	29 lqvsgttaataasvstkdpcpsqgprvpaakqcpalevtwpevnpingtlslscvacs 88	
QY	61 REPNSILYWGNGSFIEHLPGRLWEGSTSRBRGSGTQLCKALVLEOLTPLAHSTNFSK 120	
Db	89 rfpmsfilywngsfiehlpgrlwewgstsrbrgstgqlckalvleqltpalhstnfsc 148	
QY	121 VLVPDEQVVRHVVLAOLM 139	
Db	149 vlvpdeqvvrhvvlaqlm 167	
RESULT	6	
AAy83982		
ID	AAy83982 standard; Protein: 137 AA.	

```

XX AC AAT83982;
XX DT 28-JUL-2000 (first entry)
XX DE Human IL-18 binding protein 5' RACE fragment #1 encoded protein.
XX KW Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
XX KW regulator; drug; sensitivity disease; organ rejection; organ transplant;
XX KW autoimmune disease; rapid amplification of cDNA ends; RACE.
XX OS Homo sapiens.
XX WO200012555-A1.
XX PN 09-MAR-2000.
XX PD 18-NOV-1998; 98WO-JP05186.
XX PF 01-SEP-1998; 98JP-0247588.
XX PR 18-NOV-1998; 98JP-0327914.
XX PA (HAYB ) HAYASHIBARA SEIBUTSU KAKAKU.
XX PI Torigoe K, Tanai M, Kurimoto M.
XX DR WPI; 2000-237850/20.
XX DR N-PSDB: AAA11004.
XX PT Interleukin 18-binding protein with activity of regulating
PT physiological actions of interleukin 18, useful as regulator and drug
PT for sensitivily diseases and organ rejection and in treating diseases
PT due to excess immune reaction -
XX PS Example 2; Page 60-61; 71pp; Japanese.
XX CC The invention relates to novel interleukin 18 (IL-18)-binding proteins
CC from humans or mice which act as regulators and drugs for sensitivily
CC diseases and organ rejection and in treating diseases due to excess
CC immune reaction, e.g. in slowing down rejection after organ transplant,
CC and in treating autoimmune diseases. This sequence represents the
CC protein encoded by the initial fragment isolated by a 5' RACE (Rapid
CC Amplification of cDNA Ends) reaction for the 5' end of the interleukin
CC 12 binding protein coding sequence.
XX SQ Sequence 137 AA;
XX
XX Query Match 83.6%; Score 727; DB 21; Length 137;
XX Best Local Similarity 100.0%; Prid. No. 1.Ce-64;
XX Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TPVSQTTPAATAASVSRSTKDCPPSPVPFPAKKOCPALBVTWPEVEVPLNGTSLSCVACS 60
Db 1 tpvsqgtttaaasvrsstkdcpcspvpfpaakqcpalevtwpevevplngtlslscvac 60
QY 61 RFNPFSILYWLGNCSFIHLPGRLMEGSTSRBRGSGTGQLCKALVLEOUTPALNSFNFC 120
Db 61 rfnpfsilylwlgngsfiahlpgrlwegstsrergstgqlckalvlleutpalnshntisc 120
QY 121 VLVDPEOVYORHVIVLAQ 137
Db 121 vlvdpegvyvrhvvlvaq 137
XX RESULT 7
XX ID AAM98007 standard; Protein; 161 AA.
XX AC AAM98007;
XX XX
XX DT 21-JUN-1999 (first entry)
XX
```

DE Human interleukin-18 binding protein splice variant IL-18BPd.
XX
KM Interleukin-18 binding protein; IL-18BP; IL-18BPd; splice variant;
KM human; autoimmune disease; inflammation; diabetes; pancreatitis;
KM rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis;
KM psoriasis; inflammatory bowel disease; multiple sclerosis;
KM ischemic heart disease; ischemic brain injury; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..28
FT /note="signal peptide"
FT 29..161
FT Protein /note="mature protein"
XX
PN WO9909063-A1.
XX
PD 25-FEB-1999.
XX
PF 13-AUG-1998; 98WO-IL00379.
XX
PR 22-JUL-1998; 98IL-0125463.
PR 14-AUG-1997; 97IL-0121554.
PR 27-AUG-1997; 97IL-0121639.
PR 29-SEP-1997; 97IL-0121860.
PR 06-NOV-1997; 97IL-0122134.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Dinarello C, Kim SH, Novick D, Rubinstein M;
XX
DR WPI: 1999-180975/15.
DR N-PSDB; AAX24752.
XX
PT New interleukin-18 binding protein - useful for treating human
PT diseases, including autoimmune disease and inflammation
XX
PS Claim 3; Page 60; 100pp; English.
XX
CC The present sequence represents a human interleukin-18 binding
CC protein (IL-18BP) splice variant designated IL-18BPd. This is one
CC four novel splice variants (see also AAW98004-077), all putative
CC soluble proteins, that are encoded by cDNA clones (see AAX24749-52)
CC detected following a screening of human peripheral blood monocyte,
CC Jurkat T-cell, peripheral blood mononuclear cell and spleen cell
CC cDNA libraries. IL-18BPd is a low abundance variant. IL-18BP
CC polypeptides capable of binding IL-18 and/or modulating and/or
CC blocking IL-18 activity are provided, as are methods for their
CC isolation and recombinant production, DNA vectors expressing them,
CC vectors useful for their expression in humans and other mammals,
CC and antibodies against them. IL-18BP polypeptides, and DNA encoding
CC them, can be used to treat conditions requiring the protein
CC (claimed). Conditions include autoimmune diseases, type I diabetes,
CC rheumatoid arthritis, graft rejections, inflammatory bowel disease,
CC sepsis, multiple sclerosis, ischemic heart diseases, ischemic brain
CC injury, chronic hepatitis, psoriasis, and chronic/acute
CC pancreatitis. IL-18BP is also useful for purifying IL-18 (claimed).
XX
SQ Sequence 161 AA:

Query Match 60.3%; Score 525; DB 20; Length 161;
Best Local Similarity 100.0%; Pred. No. 2.4e-44;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPVSQTTAAATASVRSRKDCPSOPVFPAPAKOCPALEVTWPEVEVPLNGTSLSCVACS 60
Db 29 tpsvqttaataasvrsrkdcpsopvfpapakcpalevtwpevevplngtislscvacs 88

QY 61 RFPNFSILYWGNGSFTEHLPGRLMEGSTSRERGSTG 97
Db 89 rfpnfslilywlngsftehlpgrlmegstsrergstg 125

RESULT 8
AA83952
ID AAY83952 standard; Protein; 165 AA.
XX
AC AAY83952;
XX
DT 28-JUL-2000 (first entry)
XX
DE Mouse mature interleukin 18 binding protein.
XX
KM Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
KM regulator; drug; sensitivity disease; organ rejection; organ transplant;
KM autoimmune disease.
XX
OS Mus musculus.
XX
PN WO200012555-A1.
XX
PD 09-MAR-2000.
XX
PF 18-NOV-1998; 98WO-JP05186.
XX
PR 01-SEP-1998; 98JP-0247588.
PR 18-NOV-1998; 98JP-0327914.
XX
PA (HAYB) HAYASHIBARA SEIBUTSU KAKAKU.
XX
PI Torigoe K, Tanai M, Kurimoto M;
XX
DR WPI: 2000-237850/20.
DR N-PSDB; AAA11003.
XX
PT Interleukin 18-binding protein with activity of regulating
PT physiological actions of interleukin 18, useful as regulator and drug
PT for sensitivity diseases and organ rejection and in treating diseases
PT due to excess immune reaction
XX
PS Claim 1; Page 45; 71pp; Japanese.
XX
CC The invention relates to novel interleukin 18 (IL-18)-binding proteins
CC from humans or mice which act as regulators and drugs for sensitivity
CC diseases and organ rejection and in treating diseases due to excess
CC immune reaction, e.g. in slowing down rejection after organ transplant,
CC and in treating autoimmune diseases. This sequence represents the mature
CC mouse interleukin 12 binding protein.
XX
SQ Sequence 165 AA:

Query Match 59.2%; Score 515; DB 21; Length 165;
Best Local Similarity 66.3%; Pred. No. 2.4e-43;
Matches 105; Conservative 12; Mismatches 37; Indels 4; Gaps 3;

QY 1 TPVSQTTAAATASVRSRKDCPSOPVFPAPAKOCPALEVTWPEVEVPLNGTSLSCVACS 60
Db 1 tsapqtl-atvlgsgkdcpspsavp-tkypaldvipekevplngtislscvacs 57

QY 61 RFPNFSILYWGNGSFTEHLPGRLMEGSTSRERGSTG 120
Db 58 rfpyfslilywlngsftehlpgrlmegstsrerhntstwlhralvleelsptlrsntsc 117

QY 121 VLVNDEOVQRRHVLAQLMAGLRATLPPTQALPSSSHS 158
Db 118 lfvdpqgvagyhlllaqlwdgltkapspsqetl-sshs 154

RESULT 9
AA83989
ID AAY83989 standard; Protein; 193 AA.
XX
AC AAY83989;

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XX 28-JUN-2000 (first entry)
XX Full length mouse Interleukin 18 binding protein.
DE
XX
XX Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
KW regulator; drug; sensitivity disease; organ rejection; organ transplant;
KM autoimmune disease.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX Peptide 1..28
XX /label= signal_peptide
XX 29..193
XX Protein /label= "mature IL-18 binding protein"
XX
XX MO200012555-A1.
XX
XX 09-MAR-2000.
XX
XX 18-NOV-1998; 98WO-JP05186.
XX
XX 01-SEP-1998; 98JP-0247588.
XX 18-NOV-1998; 98JP-0327914.
XX
XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX Torioge K, Tanai M, Kurimoto M;
XX WPI: 2000-237850/20.
XX N-PSDB: AAA11011.
XX
XX Interleukin 18-binding protein with activity of regulating
XX physiological actions of interleukin 18, useful as regulator and drug
XX for sensitivity diseases and organ rejection and in treating diseases
XX due to excess immune reaction -
XX
XX Example 4; Page 67-69; 71pp; Japanese.
XX
XX The invention relates to novel Interleukin 18 (IL-18)-binding proteins
XX from humans or mice which act as regulators and drugs for sensitivity
XX diseases and organ rejection and in treating diseases due to excess
XX immune reaction, e.g. in slowing down rejection after organ transplant,
XX and in treating autoimmune diseases. This sequence represents the full
XX length mouse Interleukin 12 binding protein.
XX
XX Sequence 193 AA;
SQ
Query Match 59.2%; Score 515; DB 21; Length 193;
Best Local Similarity 66.5%; Pred. No. 2.9e-43;
Matches 105; Conservative 12; Mismatches 37; Indels 4; Gaps 3;
OY 1 TPVSQTTAAASVSTKDCPSOPVPPAKKCPALFVTPVEVPLNGTILSVCVACS 60
DB 29 tsapqt--atvlgskdpcsswspavp-ekypaldivipekevrplngltlscctacs 85
OY 61 RFPNFSILYWLNGSFIEHLPGRLMEGSTRERGSTGTOLCKALVLEQLPALHSTNFS 120
DB 86 rfpyfsilywlgngsfiehlpgrlmegstsrerhntstlwnlralvleelsplstntsc 145
OY 121 VLVPDEQVQRRHVLAQLMAGLRATLPTQALPSSHS 158
DB 146 lfvdpgvayghlllaqlwdglktapspgclt-sshs 182

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DT 28-JUN-2000 (first entry)
XX Mouse IL-18 binding protein 5' RACE fragment #1 encoded protein.
DE
XX
XX Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
KW regulator; drug; sensitivity disease; organ rejection; organ transplant;
KM autoimmune disease; rapid amplification of cDNA ends; RACE.
XX
XX Mus musculus.
XX
XX MO200012555-A1.
XX
XX 09-MAR-2000.
XX
XX 18-NOV-1998; 98WO-JP05186.
XX
XX 01-SEP-1998; 98JP-0247588.
XX 18-NOV-1998; 98JP-0327914.
XX
XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX Torioge K, Tanai M, Kurimoto M;
XX WPI: 2000-237850/20.
XX N-PSDB: AAA11008.
XX
XX Interleukin 18-binding protein with activity of regulating
XX physiological actions of interleukin 18, useful as regulator and drug
XX for sensitivity diseases and organ rejection and in treating diseases
XX due to excess immune reaction -
XX
XX Example 4; Page 65; 71pp; Japanese.
XX
XX The invention relates to novel Interleukin 18 (IL-18)-binding proteins
XX from humans or mice which act as regulators and drugs for sensitivity
XX diseases and organ rejection and in treating diseases due to excess
XX immune reaction, e.g. in slowing down rejection after organ transplant,
XX and in treating autoimmune diseases. This sequence represents the
XX protein encoded by the initial fragment isolated by a 5' RACE (Rapid
XX Amplification of cDNA Ends) reaction for the 5' end of the mouse
XX Interleukin 12 binding protein coding sequence.
XX
XX Sequence 117 AA;
SQ
Query Match 50.7%; Score 441; DB 21; Length 117;
Best Local Similarity 74.1%; Pred. No. 3.5e-36;
Matches 83; Conservative 10; Mismatches 19; Indels 0; Gaps 0;
OY 32 KQCPALFVTPVEVPLNGTILSVCVACSRRPNFSILYWLNGSRIEHLPGRLMEGSTR 91
DB 5 kypaldivipekevrplngltlscctacsrfpyfsilywlgngsfiehlpgrlkeghtr 64
OY 92 ERGSTGTOLCKALVLEQLPALHSTNFSQVLVDEQVQRRHVLAQLMAGLR 143
DB 65 ehntstlwnlralvleelsplstntscflvdpqgvayghlllaqlwdglk 116

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RESULT 11
ID AAM98005 standard; Protein: 113 AA.
AC AAM98005;
DE 21-JUN-1999 (first entry)
XX Human interleukin-18 binding protein splice variant IL-18Bpb.
XX
XX Interleukin-18 binding protein; IL-18BP; IL-18Bpb; splice variant;
KW human; autoimmune disease; inflammation; diabetes; pancreatitis;
KW rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis;
KW psoriasis; inflammatory bowel disease; multiple sclerosis;
KW ischemic heart disease; ischemic brain injury; therapy.

```

```
XX OS Homo sapiens.
XX FH Key
XX FH Peptide
XX FT Location/Qualifiers
XX FT 1..28
XX FT /note= "signal peptide"
XX FT 29..113
XX FT /note= "mature protein"
XX PN
XX PN MO9909063-A1.
XX PD
XX PD 25-FEB-1999.
XX PF
XX PF 13-AUG-1998; 98WO-IL00379.
XX PR
XX PR 22-JUL-1998; 98TL-0125463.
XX PR 14-AUG-1997; 97TL-0121554.
XX PR 27-AUG-1997; 97TL-0121639.
XX PR 29-SEP-1997; 97TL-0121860.
XX PR 06-NOV-1997; 97TL-0122134.
XX PA
XX PA (YEDA ) YEDA RES & DEV CO LTD.
XX PI
XX PI Dinarello C, Kim SH, Novick D, Rubinstein M;
XX DR
XX DR WPI: 1999-180975/15.
XX DR N-PSDB; AAX24750.
XX PT
XX PT New interleukin-18 binding protein - useful for treating human
XX PS diseases, including autoimmune disease and inflammation
XX PS Claim 3; Page 55; 100pp; English.
XX CC
XX CC The present sequence represents a human interleukin-18 binding
XX CC protein (IL-18BP) splice variant designated IL-18Bpd. This is one
XX CC four novel splice variants (see also AAW98004-07), all putative
XX CC soluble proteins, that are encoded by cDNA clones (see AAX24749-52)
XX CC detected following a screening of human peripheral blood monocyte,
XX CC Jurkat T-cell, peripheral blood mononuclear cell and spleen cell
XX CC cDNA libraries. IL-18Bpd is a low abundance variant. IL-18BP
XX CC polypeptides capable of binding IL-18 and/or modulating and/or
XX CC blocking IL-18 activity are provided, as are methods for their
XX CC isolation and recombinant production, DNA vectors expressing them,
XX CC vectors useful for their expression in humans and other mammals,
XX CC and antibodies against them. IL-18BP polypeptides, and DNA encoding
XX CC them, can be used to treat conditions requiring the protein
XX CC (claimed). Conditions include autoimmune diseases, type I diabetes,
XX CC rheumatoid arthritis, graft rejections, inflammatory bowel disease,
XX CC sepsis, multiple sclerosis, ischemic heart diseases, ischemic brain
XX CC injury, chronic hepatitis, psoriasis, and chronic/acute
XX CC pancreatitis. IL-18BP is also useful for purifying IL-18 (claimed).
XX SQ
XX SQ Sequence 113 AA;
XX
XX Query Match 29.5%; Score 257; DB 20; Length 113;
XX Best Local Similarity 98.0%; Pred No. 6.5e-18;
XX Matches 48; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 TPVSQTTTATASVRSSTKDCPSQPPVPPAKOCPALEVTWPEVEVPLN 49
DB 29 tpvsqttatatsvrsstkdcpsqpvpvpaakqcpalevtwpevevpls 77
XX
XX RESULT 12
XX AAW83984
XX ID AAW83984 standard; Protein; 47 AA.
XX AC
XX AC AAW83984;
XX XX
XX DT 28-JUL-2000 (first entry)
XX FT
XX FT Human IL-18 binding protein C-terminus.
DE
```

```
XX XX
XX KW Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
XX KW regulator; drug; sensitivity disease; organ rejection; organ transplant;
XX KW autoimmune disease; rapid amplification of cDNA ends; RACE.
XX OS
XX OS Homo sapiens.
XX PN
XX PN WO200012555-A1.
XX PD
XX PD 09-MAR-2000.
XX PF
XX PF 18-NOV-1998; 98WO-JP05186.
XX PR
XX PR 01-SEP-1998; 98JP-0247588.
XX PR 18-NOV-1998; 98JP-0327914.
XX PA
XX PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX PI
XX PI Torigoe K, Tanial M, Kurimoto M;
XX DR
XX DR WPI: 2000-237850/20.
XX DR N-PSDB; AAA11006.
XX PT
XX PT Interleukin 18-binding protein with activity of regulating
XX PT physiological actions of interleukin 18, useful as regulator and drug
XX PT for sensitivity diseases and organ rejection and in treating diseases
XX PS due to excess immune reaction
XX PS Example 2; Page 62; 71pp; Japanese.
XX CC
XX CC The invention relates to novel interleukin 18 (IL-18)-binding proteins
XX CC from humans or mice which act as regulators and drugs for sensitivity
XX CC diseases and organ rejection and in treating diseases due to excess
XX CC immune reaction, e.g. in slowing down rejection after organ transplant,
XX CC and in treating autoimmune diseases. This sequence represents the
XX CC C-terminus of the interleukin 18 binding protein encoded by the 3' end
XX CC of the gene isolated by a 3' RACE (Rapid Amplification of cDNA Ends)
XX CC reaction.
XX SQ
XX SQ Sequence 47 AA;
XX
XX Query Match 28.0%; Score 244; DB 21; Length 47;
XX Best Local Similarity 100.0%; Pred. No. 4.1e-17;
XX Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 118 FSCVLVDPEDQVGRHVYLAQLMAGLRATLPTQTGEALPSSHSPQOQG 164
DB 1 fscvlvdpegvgrhvhvylagqlmaglratlptqtgealpspspqgg 47
XX
XX RESULT 13
XX AAW98008
XX ID AAW98008 standard; Peptide; 40 AA.
XX AC
XX AC AAW98008;
XX DT 21-JUN-1999 (first entry)
XX FT
XX FT Human interleukin-18 binding protein N-terminal peptide.
XX DE
XX DE Interleukin-18 binding protein; IL-18BP; human; autoimmune disease;
XX KW inflammation; diabetes; pancreatitis; rheumatoid arthritis;
XX KW graft rejection; sepsis; chronic hepatitis; psoriasis;
XX KW inflammatory bowel disease; multiple sclerosis;
XX KW ischemic heart disease; ischemic brain injury; therapy.
XX OS
XX OS Homo sapiens.
XX AC
XX AC Key
XX AC Peptide
XX AC Location/Qualifiers
XX FT 1..28
XX FT /note= "signal peptide"
XX FT 29..113
XX FT Protein
```

FT /note= "mature protein"

XX
XX WO9909063-A1.
XX
XX 25-FEB-1999.
XX
XX 13-AUG-1998; 98WO-IL00379.
XX
XX 22-JUL-1998; 98IL-0125463.
XX 14-AUG-1997; 97IL-0121554.
XX 27-AUG-1997; 97IL-0121639.
XX 29-SEP-1997; 97IL-0121860.
XX 06-NOV-1997; 97IL-0122134.
XX
XX (YEDA) YEDA RES & DEV CO LTD.
XX
XX Dinarello C, Kim SH, Novick D, Rubinstein M;
XX WPI; 1999-180975/15.
XX
XX New interleukin-18 binding protein - useful for treating human
XX diseases, including autoimmune disease and inflammation
XX
XX Claim 1; Page 63; 100pp; English.

XX This polypeptide comprises the 40 N-terminal amino acids of human
XX interleukin-18 binding protein (IL-18BP) mature polypeptide. The
XX same 40-amino acid sequence is found at the N-terminus of 4 novel
XX IL-18BP splice variants (see AAW98004-007). IL-18BP polypeptides,
XX including the splice variants, that are capable of binding IL-18
XX and/or modulating and/or blocking IL-18 activity are provided.
XX Methods for their isolation and recombinant production, DNA vectors
XX expressing them, vectors useful for their expression in humans and
XX other mammals, and antibodies against them are also provided.
XX IL-18BP polypeptides, and DNA encoding them, can be used to treat
XX conditions requiring the protein (claimed). Such conditions
XX include autoimmune diseases, type I diabetes, rheumatoid arthritis,
XX graft rejections, inflammatory bowel disease, sepsis, multiple
XX sclerosis, ischemic heart diseases, ischemic brain injury, chronic
XX hepatitis, psoriasis, and chronic/acute pancreatitis. IL-18BP is
XX also useful for purifying IL-18 (claimed).

XX
XX Sequence 40 AA;
XX
XX

Query Match 24.0%; Score 209; DB 20; Length 40;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TPVSQTTAATASVSRSTKPCSPQPPVPAKKCCPALEVT 40
DB 1 tpvsqtttaatasvstrskpcspqppvfpakqcpalevt 40
|||||

RESULT 14
AAV12716
ID AAV12716 standard; Protein: 55 AA.
XX
XX AAV12716;
XX
XX 21-JUN-1999 (first entry)
XX
XX Human 5' EST secreted protein SEQ ID NO:306.
XX
XX Human; secreted protein; EST; expressed sequence tag; diagnosis;
XX forensic; gene therapy; chromosome mapping; signal peptide;
XX upstream regulatory sequence; cytokine activity; cell proliferation;
XX differentiation; haematopoiesis regulation; tissue growth regulation;
XX reproductive hormone regulation; chemotactic; chemokinetic; hemostatic;
XX thrombolytic; anti-inflammatory; tumour inhibition.
XX
XX Homo sapiens.
XX

PN WO9906549-A2.
XX
XX 11-FEB-1999.
XX
XX 31-JUL-1998; 98WO-IB01231.
XX
XX 01-AUG-1997; 97US-0905279.
XX
XX (GEST) GENSET.
XX
XX Duclert A, Dumas Milne Edwards J, Lacroix B;
XX WPI; 1999-153779/13.
XX
XX N-PSDB; AAX51494.
XX
XX New nucleic acids encoding human secreted proteins - obtained from
XX cDNA libraries derived from testis, ovary, uterus and spleen tissue
XX
XX Claim 34; Page 404-405; 522pp; English.

XX AAX51459 to AAX51691 represent 5' expressed sequence tags (ESTs) for
XX human secreted proteins, and encode the proteins given in AAV12681 to
XX AAV12913, respectively. The proteins given represent the signal peptide
XX and an N-terminal fragment of a secreted protein. The nucleic acid
XX sequences can be used for producing secreted human gene products. They
XX can also be used to develop products for diagnosis and therapy. The
XX proteins obtained may have cytokine activity, cell
XX proliferation/differentiation activity, haematopoiesis regulating
XX activity, tissue growth regulating activity, reproductive hormone
XX regulating activity, chemotactic/chemokinetic activity, haemostatic and
XX thrombolytic activity, receptor/ligand activity, anti-inflammatory
XX activity, tumour inhibition activity or other activities. The products
XX can be used in forensic, gene therapy and chromosome mapping procedures.
XX The sequences can also be used for obtaining corresponding promoter
XX sequences. The nucleic acids encoding the signal peptide can be used for
XX directing extracellular secretion of a polypeptide or the insertion of a
XX polypeptide into a membrane, or importing a polypeptide into a cell.

XX
XX Sequence 55 AA;
XX
XX

Query Match 14.0%; Score 122; DB 20; Length 55;
Best Local Similarity 100.0%; Pred. No. 6.7e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TPVSQTTAATASVSRSTKPCPSQ 24
DB 31 tpvsqtttaatasvstrskpcpsq 54
|||||

RESULT 15
AAV83960
ID AAV83960 standard; Protein: 29 AA.
XX
XX AAV83960;
XX
XX 28-JUL-2000 (first entry)
XX
XX Human interleukin 18 binding protein peptide fragment #8.
XX
XX Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
XX regulator; drug; sensitivity disease; organ rejection; organ transplant;
XX autoimmune disease.
XX
XX Homo sapiens.
XX
XX Key location/Qualifiers
XX MISC-difference 13..15
XX /note= "unknown amino acid"
XX MISC-difference 17..18
XX /note= "unknown amino acid"
XX
XX WO200012555-A1.
XX
XX

XX 09-MAR-2000.
 PD 18-NOV-1998; 98WO-JP05186.
 XX
 PF 01-SEP-1998; 98JP-0247588.
 XX 18-NOV-1998; 98JP-0327914.
 PR
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 PI Toriigo K, Taniai M, Kurimoto M;
 XX
 DR WPI; 2000-237850/20.
 XX
 PT Interleukin 18-binding protein with activity of regulating
 PT physiological actions of Interleukin 18, useful as regulator and drug
 PT for sensitivity diseases and organ rejection and in treating diseases
 PT due to excess immune reaction -
 XX
 PS Claim 2; Page 49; 71pp; Japanese.
 XX
 CC The invention relates to novel interleukin 18 (IL-18)-binding proteins
 CC from humans or mice which act as regulators and drugs for sensitivity
 CC diseases and organ rejection and in treating diseases due to excess
 CC immune reaction, e.g. in slowing down rejection after organ transplant,
 CC and in treating autoimmune diseases. This sequence represents a peptide
 CC fragment of the human interleukin 12 receptor protein.
 XX
 SQ Sequence 29 AA;

Query Match 13.1%; Score 114; DB 21; Length 29;
 Best Local Similarity 82.8%; Pred. No. 0.00019;
 Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 103 ALVLEQLTPALHSTNFCVLVDEPOVVQR 131
 ||||||||| | |||||||||
 Db 1 alvleqtpalhstnfcxvfvdpqvqr 29

Search completed: August 19, 2002, 22:52:56
 Job time: 3842 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 19, 2002, 22:16:04 ; Search time 24.68 Seconds
(without alignments)
162.309 Million cell updates/sec

Title: US-09-786-130-1

Perfect score: 870

Sequence: 1 TPVSGTTAATASVRSKDP.....TLPTQALPSSHSPPQGG 164

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_AA:*
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfillsl.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	106	12.2	134	1	US-08-307-499-24
2	106	12.2	134	4	US-09-299-268-24
3	96.5	11.1	579	4	US-09-173-151A-2
4	96.5	11.1	686	4	US-09-173-151A-4
5	82.5	9.5	1241	4	US-09-040-774-2
6	79	9.1	674	3	US-08-893-852A-1
7	78	9.0	216	2	US-08-715-204-7
8	78	9.0	216	2	US-09-162-597-7
9	75	8.6	1481	2	US-08-616-844-40
10	75	8.6	1481	2	US-08-599-654-40
11	75	8.6	1481	3	US-08-944-868A-40
12	75	8.6	1481	3	US-08-944-423A-40
13	75	8.6	1481	3	US-08-944-496A-40
14	73	8.5	1312	4	US-09-041-886-19
15	73	8.4	189	4	US-09-199-637A-95
16	72	8.3	280	4	US-09-247-155-178
17	71.5	8.2	1651	4	US-09-540-245A-18
18	69.5	8.0	499	4	US-09-049-672A-1
19	69	7.9	410	1	US-08-091-519-13
20	69	7.9	410	1	US-08-442-043A-13
21	69	7.9	410	5	US-09-173-151A-27
22	69	7.9	410	5	US-09-173-151A-13
23	69	7.9	410	5	US-09-173-151A-13
24	68.5	7.9	486	1	US-07-672-483-2
25	68.5	7.9	1172	1	US-08-313-288B-19
26	68	7.8	372	1	US-08-202-056-5
27	68	7.8	372	1	US-08-076-093A-6

28	68	7.8	372	1	US-08-701-265-6	Sequence 6, Appli
29	68	7.8	372	2	US-08-284-586-6	Sequence 6, Appli
30	68	7.8	372	2	US-08-805-478-6	Sequence 6, Appli
31	68	7.8	372	2	US-08-802-627A-6	Sequence 6, Appli
32	68	7.8	372	2	US-08-801-238-6	Sequence 6, Appli
33	68	7.8	372	2	US-08-801-228-6	Sequence 6, Appli
34	68	7.8	372	3	US-09-104-296-6	Sequence 6, Appli
35	68	7.8	372	3	US-08-982-493-8	Sequence 8, Appli
36	68	7.8	4302	3	US-08-658-136-5	Sequence 5, Appli
37	68	7.8	4303	2	US-08-460-751-2	Sequence 2, Appli
38	67	7.7	340	4	US-09-360-779-2	Sequence 2, Appli
39	67	7.7	374	3	US-08-982-493-6	Sequence 6, Appli
40	67	7.7	623	1	US-08-653-740-7	Sequence 7, Appli
41	67	7.7	623	2	US-09-073-594-7	Sequence 7, Appli
42	67	7.7	623	3	US-09-275-925-7	Sequence 7, Appli
43	67	7.7	1257	2	US-08-750-152A-2	Sequence 2, Appli
44	67	7.7	1449	3	US-08-840-062-6	Sequence 6, Appli
45	66.5	7.6	171	4	US-09-173-151A-18	Sequence 18, Appli

ALIGNMENTS

RESULT 1
US-08-307-499-24
; Sequence 24, Application US/08307499
; Patent No. 5651972
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Vi uela, Eladio
; APPLICANT: Gibbs, E.P.J.
; TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
; TITLE OF INVENTION: Live Vaccine Vector
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: U.S.A.
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,499
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/908,241
; FILING DATE: 1-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/908,630
; FILING DATE: 29-JUN-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/342,212
; FILING DATE: 21-APR-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF35.1.FWCC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 134 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-299-268-24

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 amino acids
; TYPE: amino acid

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;      TOPOLOGY: linear
;      MOLECULE TYPE: protein

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OY 22 PSQPVFPFAKOCPPALEVTPW---EVEVPLNGTSLISCVAGSRPFNFSTILYWGNGSFTE 78
| | | | : | | | : | | | | : | | | |
Db 239 PPGPVP-----IEMPGIDEGHVAGQSLFPCVARGNP-LATLQWLKNGQ---- 283
OY 79 HLPGLMEGSTSRERGSTGTQ-LCKALVLEQLTPALHSTNFSC----- 120
| | | | : | | | : | | | | : | | | |
Db 284 -----PVSTANGTEHTQAVARSVLVTPEDHGAQLSCGAHNSVSAGTQEHGTL 334
OY 121 -VLVDEQV-----ORHVLAQLMAGLRATLPTQEALEPSSH 157
| | | | : | | | : | | | | : | | | |
Db 335 QVTFPPSAIILIGSASQTEKNKVTLSGVSKSRPRVLLRMWLGMQQLPMEETVMDGLH 393

RESULT 6
US-08-893-852A-1
; Sequence 1, Application US/08893852A
; Patent No. 6080558
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: NEW HUMAN GROWTH REGULATOR PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/893,852A
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0341 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 674 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: TMDR3DT01
; CLONE: 508302
; US-08-893-852A-1

Query Match 9.1%; Score 79; DB 3; Length 674;
Best Local Similarity 25.9%; Pred. No. 3.4;
Matches 43; Conservative 13; Mismatches 60; Indels 50; Gaps 9;
OY 14 VRSTKDCPSQPVFPFAKQ---CPALEVTPWEVEVPLNTSLISCVAGSRPFNFS--- 66
| | | | : | | | : | | | | : | | | |
Db 513 VPGKPPPPMAPRRLPLRLQRLRKRPETPTTHDPDETFLK-----ARKVRFSEKV 562
OY 67 ---ILYWLNGSFIEHLPGRLMEGSTSRERGSTGTQ-LCKALVLEQLTPALHSTNFSCVL 122
| | | | : | | | : | | | | : | | | |
Db 563 TVHFLAVWAGFAQAAGQP---WE-QLARDSRRARITQ--QBELSPCL----- 607

OY 123 VDPEQVORHVLAQLMAGLR-----ATLPTQEALEPSSH--SSPQQ 162
| | | | : | | | : | | | | : | | | |
Db 608 -----TPARARARWARLRNPPLAPALPQLTLPSSSVSPSPVQ 645

RESULT 7
US-08-715-204-7
; Sequence 7, Application US/08715204
; Patent No. 5874286
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Au-Yang, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer.
; APPLICANT: Zweiger, Gary B.
; TITLE OF INVENTION: A NOVEL TUMOR PROTEIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/715,204
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0126 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 216 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: Genbank
; CLONE: 470373
; US-08-715-204-7

Query Match 9.0%; Score 78; DB 2; Length 216;
Best Local Similarity 26.8%; Pred. No. 0.9;
Matches 26; Conservative 16; Mismatches 37; Indels 18; Gaps 4;
OY 54 LSCVACSRFPNFSILYWLNGSFIEHLPGRLMEGSTSRERGSTGTQ-LCKALVLEQLTPAL 113
| | | | : | | | : | | | | : | | | |
Db 7 INCFLAPAFYFIYKYSGINEY-----SSIMKATA-SGGYLLTLQAKLLIATFFPAL 60
OY 114 HSTNPSCVLVDPE-----QVVORHVLAQLMAG 141
| | | | : | | | : | | | | : | | | |
Db 61 DSEGEISY---PEFLKSSADIIIVIGLHLLMTNPLAG 94
RESULT 8
US-09-162-597-7
; Sequence 7, Application US/09162597
; Patent No. 6043343

GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
APPLICANT: Goll, Surya K.
APPLICANT: Hillman, Jennifer.
APPLICANT: Zweiger, Gary B.
TITLE OF INVENTION: A NOVEL TUMOR PROTEIN
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/162,597
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/715,204
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0126 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 216 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 470373
US-09-162-597-7

Query Match 9.0%; Score 78; DB 3; Length 216;
Best Local Similarity 26.8%; Pred. No. 0.9;
Matches 26; Conservative 16; Mismatches 37; Indels 18; Gaps 4;

QY 54 LSCVACSRPFNFSILYMWGSGFIEHLPGRLMGSTSRERGSGTQQLCKALVLEQLPAL 113
DB .7 INFALAFAPYFTVYKISGINY-----SITWCATRA-SCGYLLTOLAKLITATFPAL 60

QY 114 HSTNFSCLVDP-----QVORHVYLAQLMAG 141
DB 61 DSEGSFIV---PEFLKSSADIIDVIGLHLMTFMFLAG 94

RESULT 9
US-08-616-844-40
Sequence 40, Application US/08616844
Patent No. 5849578
GENERAL INFORMATION:
APPLICANT: FALB, DEAN A.
TITLE OF INVENTION: COMPOSITION AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York

COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/616,844
FILING DATE: 15-MAR-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,654
FILING DATE: 09-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,573
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: CORUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1481 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-616-844-40

Query Match 8.6%; Score 75; DB 2; Length 1481;
Best Local Similarity 23.8%; Pred. No. 27;
Matches 57; Conservative 18; Mismatches 78; Indels 86; Gaps 10;

QY 2 PVSOTT-TAATASVSRKDCPCSPVPVPAKOCPALEV----- 39
DB 820 PVSLLTTSAPLSVSQTLTQSSSTPYLPARRETPVTSFOTSTVTSWMTLHSSQTDALK 879

QY 40 --TWPEYEVPLNGTSLSCVACSRFPNFSILYMWGSGFIEHLPGRLMGSTSRERGSGT 97
DB 880 SOSTPHQEKVITEKSPSLVS---LPTESTKAVTTNSP---LPSSLTESSTEQTLDPATS 932

QY 98 TQCK-----ALVLE-----QLTPALHSTNFSY-----LYDEQVY-- 129
DB 933 TNLQMSPTFTTTLTKLSQPLMTPTGLTSLSTASLVTGPPIAVQTTAGKQLSTHPELIVPQ 992

QY 130 -----ORHVLAQLMAGL-----RATLPPTOALPSSHS-----SPQ 161
DB 993 ISTEGISTERNYIVATGTGLPITSVPTSAREMTTKLGVTATAYSPASNSLGTSPPQ 1051

RESULT 10
US-08-599-654-40
Sequence 40, Application US/08599654
Patent No. 5882925
GENERAL INFORMATION:
APPLICANT: FALB, DEAN A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York

COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,654
FILING DATE: 09-FEB-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,573
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: CORUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1481 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-599-654-40

Query Match 8.6%; Score 75; DB 2; Length 1481;
Best Local Similarity 23.8%; Pred. No. 27;
Matches 57; Conservative 18; Mismatches 78; Indels 86; Gaps 10;

QY 2 PVSQTT-TAATASVSTNDPCSPQPPVPPAAKCPALEV----- 39
DB 820 PVSLLTSTAPLSVSQTLTPQSSSTPVLPRARETPVTSFQSTMTSFMTHLSQADLK 879
QY 40 --TWPEVEVPLNGTSLSCVACSRPNFSILWLGNSFIEHLPRLMGSTRRGSG 97
DB 880 SOSTPHQEKVITRESKPSLVS---LPTESTKAVTTNSP---LPPLSTESSSTEOPLPATS 932
QY 98 TOLCK-----ALVLE-----OLTPALHSTNFCV-----LVDPQOV-- 129
DB 933 TNLQMSPTFTTILKTSQPLMTTPGTLSTASLVTPGPIAVQTAGKQLSLTHPELIVPQ 992
QY 130 -----QRHVYLAQLMAGL-----RATLPPTQELPSSH-----SPQ 161
DB 993 ISTEGLISTERNRVIVDATGTGLIPLTSVPTSAKEMTKLGVTAEYSPASRSLSGTSPSPQ 1051

RESULT 11
US-08-944-868A-40
Sequence 40, Application US/08944868A
Patent No. 6018025
GENERAL INFORMATION:
APPLICANT: FALB, DEAN A
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,868A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/599,654
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: CORUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1481 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-944-868A-40

Query Match 8.6%; Score 75; DB 3; Length 1481;
Best Local Similarity 23.8%; Pred. No. 27;
Matches 57; Conservative 18; Mismatches 78; Indels 86; Gaps 10;

QY 2 PVSQTT-TAATASVSTNDPCSPQPPVPPAAKCPALEV----- 39
DB 820 PVSLLTSTAPLSVSQTLTPQSSSTPVLPRARETPVTSFQSTMTSFMTHLSQADLK 879
QY 40 --TWPEVEVPLNGTSLSCVACSRPNFSILWLGNSFIEHLPRLMGSTRRGSG 97
DB 880 SOSTPHQEKVITRESKPSLVS---LPTESTKAVTTNSP---LPPLSTESSSTEOPLPATS 932
QY 98 TOLCK-----ALVLE-----OLTPALHSTNFCV-----LVDPQOV-- 129
DB 933 TNLQMSPTFTTILKTSQPLMTTPGTLSTASLVTPGPIAVQTAGKQLSLTHPELIVPQ 992
QY 130 -----QRHVYLAQLMAGL-----RATLPPTQELPSSH-----SPQ 161
DB 993 ISTEGLISTERNRVIVDATGTGLIPLTSVPTSAKEMTKLGVTAEYSPASRSLSGTSPSPQ 1051

RESULT 12
US-08-944-423A-40
Sequence 40, Application US/08944423A
Patent No. 6020463
GENERAL INFORMATION:
APPLICANT: FALB, DEAN A
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS 95

```
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,423A
FILING DATE: 06-OCT-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,654
FILING DATE: 09-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,573
FILING DATE: JUN-07-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: CORUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1481 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-944-423A-40
```

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Query Match      8.6%; Score 75; DB 3; Length 1481;
Best Local Similarity 23.8%; Pred. No. 27;
Matches 57; Conservative 18; Mismatches 78; Indels 86; Gaps 10;

QY 2 PVSQTT-TAATASVRSKTPCPSPQPVFPAPAKCCPALEV----- 39
DB 820 PVSLLTSTAPLSVSGTTLQSSSTVPLPRAREPVTSPFTSMTSPMTLHSSQTADLK 879
QY 40 --TWPEVEVPLNGTSLSCVACSRFPNFSILYWLNGSFTEHLPGRLMEGSTREKSGTG 97
DB 880 SOSTPHQEKVITESKSPSLVS--LPTESTKAVTTNSP---LPPSLTESSTEQTLPAT 932
QY 98 TOLCK-----ALYLE-----QLTPALHSTNFCV-----LYDEQVY-- 129
DB 933 TNLQMSPTTTTLTKTSQPLMTTPGLSTSLASLVGPIAVQTTAGKQLSLTHPELIVPQ 992
QY 130 -----QRHVLAQLMAGL-----RATLPPTOEALPSSH-----SPQ 161
DB 993 ISTEGLSTERNRNVIYDATGILPLTSVPTSAKEMTKLGVTAEYSPANSLSGTSPSPQ 1051
```

```
RESULT 13
US-08-944-496-40
Sequence 40, Application US/08944496
Patent No. 6124433
GENERAL INFORMATION:
APPLICANT: PALB, DEAN A
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,496
FILING DATE: 06-OCT-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,654
FILING DATE: 09-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,573
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: CORUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1481 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-944-496-40
```

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Query Match      8.6%; Score 75; DB 3; Length 1481;
Best Local Similarity 23.8%; Pred. No. 27;
Matches 57; Conservative 18; Mismatches 78; Indels 86; Gaps 10;

QY 2 PVSQTT-TAATASVRSKTPCPSPQPVFPAPAKCCPALEV----- 39
DB 820 PVSLLTSTAPLSVSGTTLQSSSTVPLPRAREPVTSPFTSMTSPMTLHSSQTADLK 879
QY 40 --TWPEVEVPLNGTSLSCVACSRFPNFSILYWLNGSFTEHLPGRLMEGSTREKSGTG 97
DB 880 SOSTPHQEKVITESKSPSLVS--LPTESTKAVTTNSP---LPPSLTESSTEQTLPAT 932
QY 98 TOLCK-----ALYLE-----QLTPALHSTNFCV-----LYDEQVY-- 129
DB 933 TNLQMSPTTTTLTKTSQPLMTTPGLSTSLASLVGPIAVQTTAGKQLSLTHPELIVPQ 992
QY 130 -----QRHVLAQLMAGL-----RATLPPTOEALPSSH-----SPQ 161
DB 993 ISTEGLSTERNRNVIYDATGILPLTSVPTSAKEMTKLGVTAEYSPANSLSGTSPSPQ 1051
```

```
RESULT 14
US-09-041-886-19
Sequence 19, Application US/09041886
Patent No. 6235872
GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1312 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-041-886-19

Query Match 8.5%; Score 74; DB 4; Length 1312;
Best Local Similarity 26.7%; Pred. No. 30;
Matches 47; Conservative 20; Mismatches 75; Indels 34; Gaps 9;

QY 2 PVSQTTAATAASVSTKDPK-PSQPPPPAKQCPALEVTWPEVPLNGTILSLCVACS 60
DB 570 PNSTLPPRAATPPRPPSRPPSRPSHSAHSPAPVSTMPK-RMSSEGPSPRMSPKAQR 628
QY 61 REPNSILYWLGNCS-----FIEHLPGRLMEGST--SRKSGTGTOLCKALVLEQLTP 111
DB 629 HPRNRHVS--AGRGSISSGLEFVSHNPPS--EAAIPVARTSPSGTWSVVYSGVPRLSP 684
QY 112 ALHSTNFCVLDPEQVYQRHV-----VLAQLMAGLRATLPQOALPSSHSSP 160
DB 685 KTHR-----PRSPRQNSIGNTPSGPVLASPQAGT---IPTNAVAMPITPAASP 728

RESULT 15
US-09-199-637A-95
; Sequence 95, Application US/09199637A
; Patent No. 6355411
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick
; APPLICANT: Goodman, Howard M.
; APPLICANT: Rahme, Laurence G.
; APPLICANT: Mahajan-Miklos, Shalina
; APPLICANT: Tan, Man-wah
; APPLICANT: Cao, Hui
; APPLICANT: Drenkard, Eliana
; APPLICANT: Tsongalis, John
; TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
; FILE REFERENCE: 00786/361002
; CURRENT APPLICATION NUMBER: US/09/199,637A
; CURRENT FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/066,517
; PRIOR FILING DATE: 1997-11-25
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-95

Query Match 8.4%; Score 73; DB 4; Length 189;
Best Local Similarity 23.4%; Pred. No. 2.6;
Matches 44; Conservative 20; Mismatches 64; Indels 60; Gaps 10;

QY 1 TPVSGTTAATAASVSTKDPKPPVPPAKQCPALEVTWPEVPLNGTILSLCVACS 60

DB 24 SPASATTAASA-----PASTACSPAALRLAA-----SATPALAFSCS 63
QY 61 REPNSILYWLGNCS-----FIEHLPGRLMEGST--SRKSGTGTOLCKALVLEQLTP 104
DB 64 SW-NFQTSMAHSGSNATRIPTHLPSHGLSSDIAVARSSSPTRNQRKSKMDGMLGAS 122
QY 105 -----VLEQLTPALH-----STNFCVLDPEQVYQRHVYLAQLMAG--LRATLPPTQ 150
DB 123 SSPGCVLPPTASISAHSAALSKSKSNF---FTSPRSIEYRP-----WTADVFPPLLAFTK 173
QY 151 EALPSSHS 158
DB 174 IEISSSS 181

Search completed: August 19, 2002, 22:53:42
Job time: 2258 sec


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QY 106 LEQLTPA-----LHSTNFSCVLDPQGVQRHVLQAQLMAGLRATLPP 148
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 239 VSQASPGWICVRHGOSEML-----HQRMMVALAVLAA--RCQLPP 278
```

RESULT 11
T37190

nephurin - human
C:Species: Homo sapiens (man)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C:Accession: T37190
R:Kestila, M.; Lehtkeri, U.; Mannikko, M.; Lamerdin, J.; McCreedy, P.; Putaala, H.; Ruotason, K.

Molecular Cell 1, 575-582, 1998
 A:Title: Positionally cloned gene for a novel glomerular protein - nephrin - is mutated
 A:Reference number: 221629; MUID:98325371
 A:Accession: T37190
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1241 <KES>
 A:Cross-references: EMBL:AF035835; NID:g3025698; PIDN:AC039687.1; PID:g3025699
 C:Genetics:
 A:Gene: NPHS1
 A:Map position: 19
 A:Note: mutated in congenital nephrotic syndrome of the Finnish type (NPHS1); located in

Query Match	9.5%	Score 82.5;	DB 2;	Length 1241;
Best Local Similarity	21.2%;	Pred. No. 18;		
Matches 38; Conservative	16;	Mismatches	58;	Indels 67; Gaps 7;

QY 22 PSQPEVFPAAKQCPALEVWTP--EVEVPLNGTSLSCVACSRPNFSILYWLGNCSFIE 78
| ||| | | : || ||| | : || |||

79	HLPEGLMEGSTRERKSTGTQ-LCKALVEQLTPALHSTNESC-----	12
OY		

Db 284 -----PVTAMGTEHTQAVARSLVLMVVRPEDHGAQLSCEAHNSVSAGTQEHGITL 33

335 QVTEPPSAIIILGSASOTENKNVTLSCVSKSSRPVLLRWVIGWROLLEMEETVNDGIH 393

RESULT 12

scavenger receptor cysteine-rich protein homolog srcrm2 - *Geodia cydonium*
110024

```
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-May-2000
C/Accession: T18524
C/Blumbach, B.: Pancer, Z.; Diehl-Seifert, R.; Steffan, P.; Muenzner, T.:
```

U. Cell Sci 111, 2635-2644, 1998

A:Title: The putative sponge aggregation receptor: Isolation and character

Reference number: Z18947: MIMD.98369060

A;Accession: T18524
A;Status: preliminary;
Molecule type: mRNA
translated from GB/EMBL/DBJ

A;Residues: 1-2043 <BLD>
A;Cross-references: EMBL:Y14953; NID:e1364818; PID:e1364819; PIDN:CAA7517
Genetics:

A; Gene: SRCRM2

Query Match	9.5%;	Score 82.5;	DB 2;	Length 2043;
Best Local Similarity	23.1%;	Pred. No. 31;		

21 CPSQPVFPAKQCPAL----EVTWPEVEVPLNGTSLSCVACSRFPNFSILYWLNGSF 76

Db 1765 CSREPT-----KCPTLTISDHWLASSETTINTVVSFTC-----DNGYFLKGDKI 18

[illegible]

Db 1811 LECISTGVWNGTAFT---CSLPNSCPELKSIDHVTASTDTDRINAVVFTCCDDRYTLNG 1864

Qy 132 HWVLA----QLMAGLRAT---LPPTQELALPSSHSP 160

Db 1868 NKIIACQSTGVWNGSTAPCTCKEITPCELPPSSVHP 1903

RESULT 13

T27123
hypothetical protein Y53C10A.10 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_revision 15-Oct-1999
C:Accession: T27123
R:White, S
Submitted to the EMBL Data Bank on November 1999

Submitted to the EMBL Data Library, November 1996
 A:Reference number: Z20314
 A:Accession: T27123
 A:Status: preliminary; translated from GR/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-627 <MIL>
 A:Cross-references: EMBL:AL033536; PIDN:CAA22144.1; CESP:Y53C10A.10
 A:Experimental source: clone Y53C10A
 C:Genetics:
 A:Gene: CESP:Y53C10A.10
 A:Introns: 12/1; 82/1; 102/1; 131/1; 181/1; 212/1; 236/3; 308/3; 351/3; 382/3; 426/1

Query Match	9.3%	Score 81	DB 2	Length 627
Best Local Similarity	24.5%	Pred. No. 11		
Matches 39	Conservative 20	Mismatches 40	Indels 60	Gaps 8

QY 20 PCPSOPVFPAAKQCPALEVTWPEVEVEPLNGTSLSCVACSRFPNFSILYMGNGS----- 75

02 76 --FLEHLPGR--LMEGSTSRERGSTQJLCAVLLEOLTPALHSTNFCVLPDEPQWQ 130

```

Db      404  VLLLEVLPGGGVIRNCTDSKDE-SSCSLSKS-----TPSFLSPFTDS----- 445

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```

QY 131 KHVLAQLMAGLKAIP-----IQEALPSSHSSP 160
      | | | | | : : : | | |
Db 446 -----LTATPPGSGITOAASSTESAMASSIESP 473

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RESULT 14

T17158
CL2AB protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T17158
R:Sugita, S.; Ichchenko, K.; Khvochev, M.; Sudhof, T.C.

A;Description: CL family.
A;Reference number: Z18712

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA

A; Cross-references: EMBL:AF081149; NID:g3695124; PID:g3695125; PIDN:AAC62655.1
C; Superfamily: alpha-latrotoxin receptor, calcium-independent

Query Match 9.38; Score 81; DB 2; Length 1420

25.00; *freq*: NO. 25;
 38; Conservative 20; Mismatches 48; Indels 54; Gaps 10;

433 PVSSTVAGPQEGSGKTPPPAVSTTKIPVTNIFPLPERECEALFMKGKMPOTORGMMV 4922

QY 45 EYP---LNGTSLSCVACS-----RFPNFS--ILTYIGN-----GSFIE 78
| | | | |
| | | | |

D6 493 ERDCEKGTGTAASYLCMASTGTWNEKGPDLNCTSHWVNLQAKIRSGENNAASLANELAK 552

```

QY      79 HHPGRMEGSGTSRERGSGTGDTOLKALV-----LEQITPA 112
      | | :: | | : : | | | : : | |
Db      553 HFKGTVPAGDV-----SSSVRLMEQLVDILDAQQLKPS 587

```

RESULT 15

CL2B8 protein - rat
 C1:Species: Rattus norvegicus (Norway rat)
 C2:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 04-Mar-2000
 C3:Accession: T46611
 R1:Sigita, S.; Ichtchenko, K.; Khvotchev, M.; Sudhof, T. C.
 submitted to the EMBL Data Library, July 1998
 A3:Description: CL family.
 A1:Reference number: z18712
 A2:Accession: T46611
 A4:Status: preliminary; translated from GB/EMBL/DBJ
 A5:Molecule type: mRNA
 A6:Residues: 1-1435 <SUG>
 A7:Cross-references: EMBL:AF081152; NID:g3695130; PID:g3695131; PRIDN:AAC62658.1.1
 C4:Superfamily: alpha-latrotoxin receptor, calcium-independent

		9.3%;	Score 81;	DB 2;	Length 1435;
		Best Local Similarity	23.8%;	Pred. No. 29;	
		Matches 38;	Conservative 20;	Mismatches 48;	Indels 54; Gaps 10;
OY	2	PVSQTTAAATASVSTKDP-----CPSOPFPFAAK-CPALE-----VTWDE-----V	44		
		: : : :			
Dd	433	PVSSVAGPQGSGSKGTTPRAVSTTKIRPVNINIFLPERFCALEMKGIGKWQTGRGMNV	492		
OY	45	EVP-----LNGTLLSLSCVACS-----RPFNFES--ILYWLGN-----GSFIE	78		
		: : : :			
Dd	493	ERPCKPTGRTGAASYLCMASTGTWNPKGPDLSNCTSHMWYNQLAQKTRSGENNAASLANELAK	552		
OY	79	HLPGRLMEGSTSRKSGSTGTCQLCKALV-----LEQLPLRA	112		
		: : : : : : : : : : :			
Dd	553	HTKGVTFAGDV-----SSSVRLMDLVLIIDLAQLOELKPS	587		

Search completed: August 19, 2002, 22:54:46
Job time: 472 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 19, 2002, 22:52:59 ; Search time 23.86 Seconds

(without alignments)
266.136 Million cell updates/sec

Title: US-09-786-130-1
Perfect score: 870
Sequence: 1 TPVSGTTTAAATVAFVSTKDP.....TLPTQALPSSHSPPQOG 164

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt-40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74.2	85.3	197	118B_HUMAN	O95998 homo sapien
2	106	12.2	134	1VC09_SPKA	P32223 swinepox vi
3	83	9.5	370	PUS2_YEAST	P53167 saccharomyc
4	81	9.3	823	DMSA_RHOCA	052675 rhodobacter
5	78.5	9.0	2594	71ES_DROVI	P20806 drosophila
6	77.5	8.9	754	MBPL_KIOLA	P39679 Kluveromyc
7	76.5	8.8	1914	1KMUS_HUMAN	Q15746 homo sapien
8	76	8.7	374	CCR5_RAT	P34997 rattus norv
9	75.5	8.7	505	1CXAA_MOUSE	O92794 rattus norv
10	75.5	8.7	2004	1MOZ_HUMAN	O92794 rattus norv
11	74.5	8.6	416	1ILIS_RAT	P43303 rattus norv
12	74.5	8.6	3511	1MY15_MOUSE	O94924 mus musculu
13	73.5	8.4	353	1ALCI_HUMAN	P01876 homo sapien
14	73.5	8.4	1172	1TSP2_MOUSE	O03350 mus musculu
15	73	8.4	1538	1LHR_ECOLI	P30015 escherichia
16	73	8.4	3415	1POLG_MOUSE	O04538 t genome po
17	72.5	8.3	456	1GUNA_MICBI	P26414 microbisp
18	72	8.3	886	1YFIO_ECOLI	P76594 escherichia
19	71.5	8.2	423	1GATM_MOUSE	O94964 mus musculu
20	71.5	8.2	780	1NH48_CAEEL	O94407 caenorhabd
21	71.5	8.2	2688	1ZEPI_MOUSE	O03172 mus musculu
22	70.5	8.1	353	1ALCI_GORGO	P20758 gorilla gor
23	70.5	8.1	633	1CNEI_HUMAN	O90166 homo sapien
24	70	8.0	2090	1HREL_MESAU	P51611 mesocricetu
25	69.5	8.0	583	1HEMO_BRARE	O94914 brachydanio
26	69.5	8.0	4590	1FATR_HUMAN	O14517 mus musculu
27	69	7.9	410	1ILIS_MOUSE	P27931 mus musculu
28	68.5	7.9	423	1GATM_RAT	P50442 rattus norv
29	68.5	7.9	486	1ENV_HTLV2	P03383 human t-cel
30	68.5	7.9	1172	1TSP2_MOUSE	P35442 homo sapien
31	68	7.8	372	1CCR5_HUMAN	P32302 homo sapien
32	68	7.8	626	1MAG_HUMAN	P20916 homo sapien
33	68	7.8	1257	1KPBA_CAEEL	P34335 caenorhabd

34	68	7.8	4303	1PKD1_HUMAN	P98161 homo sapien
35	67.5	7.8	354	1YJFR_ECOLI	P39300 escherichia
36	67.5	7.8	488	1ENV_HTLIF	O03817 human t-cel
37	67.5	7.8	488	1ENV_HTLIM	P23064 human t-cel
38	67.5	7.8	488	1ENV_HTLIN	O03816 human t-cel
39	67.5	7.8	976	1KEMS_MOUSE	O00495 rattus norv
40	67.5	7.8	978	1KEMS_RAT	O00495 rattus norv
41	67.5	7.8	1025	1HIRA_FUGRU	O42611 fugu rubrip
42	67.5	7.8	1522	1BAI3_HUMAN	O60242 homo sapien
43	67	7.7	374	1CCR5_MOUSE	O04683 mus musculu
44	67	7.7	564	1PKNA_ANASP	P54734 anabena sp
45	67	7.7	690	1TOP1_BACHD	O9ka23 bacillus ha

ALIGNMENTS

RESULT	1	STANDARD:	PRT:	197 AA.
ID	118B_HUMAN	O95998: O95993:		
AC	O95998: O95993: O95993:			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Interleukin-18 binding protein precursor (IL-18BP).			
GN	IL18BP.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
NCBI_Taxid=9606;				
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-99146382; PubMed-10023777;			
RA	Novick D., Kim S.-H., Fantuzzi G., Reznikov L.L., Dinarello C.A.,			
RT	Rubinstein M.,			
RT	"Interleukin-18 binding protein: a novel modulator of the Th1 cytokine			
RL	response.";			
RL	Immunity 10:127-136(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-99192308; PubMed-10094485;			
RA	Alizawa Y., Akita K., Tanai M., Torigoe K., Mori T., Nishida Y.,			
RT	Ushio S., Nukada Y., Tanimoto T., Ikegami H., Ikeda M., Kurimoto M.,			
RT	"Cloning and expression of interleukin-18 binding protein.";			
RL	FEBS Lett. 445:338-342(1999).			
CC	-1- FUNCTION: FUNCTIONS AS AN INHIBITOR OF THE EARLY TH1 CYTOKINE			
CC	RESPONSE.			
CC	-1- SUBUNIT: BINDS TO IL-18.			
CC	-1- SUBCELLULAR LOCATION: Secreted (Potential).			
CC	-1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: A/IL-18BP, B/IL-18BP AND C/IL-			
CC	18BP (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.			
CC	-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.			
CC	-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL; AF110798; AAD17187.1; -			
DR	EMBL; AF110798; AAD17188.1; -			
DR	EMBL; AF110798; AAD17189.1; -			
DR	EMBL; AF110799; AAD17190.1; -			
DR	EMBL; AF110800; AAD17191.1; -			
DR	EMBL; AF110801; AAD17192.1; -			
DR	EMBL; AF110801; AAD17192.1; -			
DR	InterPro: IPR003006; Ig_MHC.			
DR	PIfam: PF00047; 19; 1.			
DR	Immunoglobulin domain; Glycoprotein; Signal; Alternative splicing.			
FT	SIGNAL 1 28 POTENTIAL.			

FT CHAIN 29 197 INTERLEUKIN-18 BINDING PROTEIN.
 FT DOMAIN 77 155 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 84 148 BY SIMILARITY.
 FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VANSPLIC 168 197 VSPRGRQGEDEELCFHMGKGGGLQSSSL -> AGLRATL
 FT VANSPLIC 77 113 PPTQALPSSHSSPOQOG (IN ISOFORM A).
 FT VANSPLIC 77 113 NGTLISLSCVACSRFPNFSILYWLNGSFIEHLPGRIW ->
 FT VANSPLIC 77 113 SWAEGNLAPHRSPALQPOQSTAAQLRLSTGPAQAOP (IN
 FT VANSPLIC 77 113 ISOFORM B).
 FT VARSPLIC 114 197 MISSING (IN ISOFORM B).
 FT SEQUENCE 197 AA: 21698 MW: 21698 MD: FLDE626AB2B285E1 CRC64:

Query Match 85.3%; Score 742; DB 1; Length 197;
 Best Local Similarity 100.0%; Pred. No. 1.8e-66;
 Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPVSTTTAATASVSTKDPSPVPVPAKOCALVETWPEVEVPLNGTSLSCVACS 60
 DB 29 TPVSTTTAATASVSTKDPSPVPVPAKOCALVETWPEVEVPLNGTSLSCVACS 88
 QY 61 RFPNFSILYWLNGSFIEHLPGRLMEGSTSRERGSTGTOLCALVLEQLPALHSTNESC 120
 DB 89 RFPNFSILYWLNGSFIEHLPGRLMEGSTSRERGSTGTOLCALVLEQLPALHSTNESC 148
 QY 121 VLVDPEQVQVRHVVLAQLM 139
 DB 149 VLVDPEQVQVRHVVLAQLM 167

RESULT 2
 VC09-SPVKA STANDARD; PRT: 134 AA.
 ID VC09-SPVKA
 AC P33223;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Hypothetical protein C9.
 GN C9L.
 OS Swinepox virus (strain Kasza) (SPV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Suipoxvirus.
 OX NCBI_TaxID=10277;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9406924; PubMed=8249275;
 RA Messing R.F., Jayarama V., Moyer R.W.;
 RT "DNA sequence analysis of conserved and unique regions of swinepox
 RT virus: identification of genetic elements supporting phenotypic
 RT observations including a novel G protein-coupled receptor
 RT homologue.";
 RL Virology 197:511-528(1993).
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 CC
 DR EMBL: L22013; AAC37862.1; -;
 DR Hypothetical protein.
 KW SEQUENCE 134 AA: 15811 MW: F3528BB783ED1DC4 CRC64:

Query Match 12.2%; Score 106; DB 1; Length 134;
 Best Local Similarity 28.4%; Pred. No. 0.001;
 Matches 27; Conservative 20; Mismatches 42; Indels 6; Gaps 3;

QY 57 VACSRFPN--FSTLYWL--GNGSFIEHLPGRLMEGS--TSRERGSTGTOLCALV
 DB 38 VACNGYNTSTSYLTYWVGNNTFEQDLNSDHYKKEKYNSTERNHEMYRLTDLII
 QY 111 PALHSTNFSVCVLDPEQVQVRHVVLAQLMAGLRAT 145
 DB 98 SEMEMTKLTVCVLSDIYTPIKASTILNLMWCLNPTT 132

RESULT 3
 PUS2_YEAST STANDARD; PRT: 370 AA.
 ID PUS2_YEAST
 AC P53167; Q06713;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Pseudouridylate synthase 2 (EC 4.2.1.70) (Pseudouridine synthase 2).
 GN PUS2 OR YG1063W.
 OS Saccharomyces cerevisiae (baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96208513; PubMed=8641292;
 RA Simos G., Tekotte H., Grosjean H., Segref A., Sharma K., Tollervey D.,
 RA Hurt E.C.;
 RT "Nuclear pore proteins are involved in the biogenesis of functional
 RT tRNA.";
 RL EMBO J. 15:2270-2284(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RX MEDLINE=97377993; PubMed=9234674;
 RA Feuerhann M., de Montigny J., Potier S., Souciet J.-L.;
 RT "The characterization of two new clusters of duplicated genes
 RT suggests a 'lego' organization of the yeast Saccharomyces cerevisiae
 RT chromosomes.";
 RL Yeast 13:861-869(1997).
 CC -1- FUNCTION: FORMATION OF PSEUDOURIDINE IN THE ANTICODON STEM AND
 CC LOOP OF TRANSFER RNAs.
 CC -1- CATALYTIC ACTIVITY: Uracil + D-ribose 5-phosphate -> pseudouridine
 CC 5'-phosphate + H(2O).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE TRNA FAMILY OF PSEUDOURIDINE SYNTHASES.
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 CC
 DR EMBL: X80674; CAA56699.1; -;
 DR EMBL: Z72585; CAA96766.1; -;
 DR SGD: S0003031; PUS2.
 DR InterPro: IPR001406; Pseudou_synth_1.
 DR Pfam: PF01416; Pseudou_synth_1; 1.
 KW Lysase; tRNA processing; Nuclear protein.
 FT CONFLICT 136 136 C -> S (IN REF. 2).
 SO SEQUENCE 370 AA: 41891 MW: 776D3A5D8C83EBG3 CRC64:

Query Match 9.5%; Score 83; DB 1; Length 370;
 Best Local Similarity 29.6%; Pred. No. 0.68;
 Matches 32; Conservative 18; Mismatches 36; Indels 22; Gaps 6;

QY 48 LNSTLSVCVACSRFPN--SILYWLNGSFIEHLPGRLMEGSTSRERGSTGTOLCALV 105
 DB 186 LNSTLSVCVACSRFPN--SILYWLNGSFIEHLPGRLMEGSTSRERGSTGTOLCALV 105
 DB 106 LEQLTPA-----LHSTNFSVCVLDPEQVQVRHVVLAQLMAGLRATLP 148

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Db 239 VSOASPGWICVIRHGOSEFML-----HQIRRMVALAVLAA--RCOLBP 278

RESULT 4
DMSA_RHOCA STANDARD; PRT; 823 AA.
ID DMSA_RHOCA 052675;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Dimethyl sulfoxide reductase precursor (EC 1.8.99.-) (DMSO reductase)
DE (DMSOR).
GN DORA.
OS Rhodobacter capsulatus (Rhodospseudomonas capsulata).
OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
OC Rhodobacter.
OX NCBI_TaxId=1061;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 43-59.
RC STRAIN-DSM 938 / 37B4;
RX MEDLINE=97008997; PubMed=8856102;
RA Shaw A.L., Hanson G.R., McEwan A.G.;
RT Cloning and sequence analysis of the dimethylsulfoxide reductase
RT structural gene from Rhodobacter capsulatus.";
RL Biochim. Biophys. Acta 1276:176-180(1996).
RN [2]
RP REVISIONS.
RA Shaw A.L., McEwan A.G.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.88 ANGSTROMS).
RX STRAIN-DSM 938 / 37B4;
RA MEDLINE=97045990; PubMed=8890912;
RA Schneider F., Loewe J., Huber R., Schindelin H., Kisker C.,
RA Knaeblein J.;
RT "Crystal structure of dimethyl sulfoxide reductase from Rhodobacter
RT capsulatus at 1.88-A resolution.";
RL J. Mol. Biol. 263:53-69(1996).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RC STRAIN-H123;
RA McAlpine A.S.;
RT "Molybdenum active centre of DMSO reductase from Rhodobacter
RT capsulatus: crystal structure of the oxidised enzyme at 1.82-A
RT resolution and the dithionite-reduced enzyme at 2.8-A resolution.";
RL J. Biol. Inorg. Chem. 2:690-700(1997).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RC STRAIN-H123;
RX MEDLINE=20296793; PubMed=10835270;
RA Stewart L.J., Bailey S., Bennett B., Charnock J.M., Garner C.D.,
RA McAlpine A.S.;
RT "Dimethylsulfoxide reductase: an enzyme capable of catalysis with
RT either molybdenum or tungsten at the active site.";
RL J. Mol. Biol. 299:593-600(2000).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RC STRAIN-H123;
RX MEDLINE=20442077; PubMed=10985771;
RA Bray R.C., Adams B., Smith A.T., Bennett B., Bailey S.;
RT "Reversible dissociation of thiolate ligands from molybdenum in an
RT enzyme of the dimethyl sulfoxide reductase family.";
RL Biochemistry 38:11258-11269(2000).
CC -1- FUNCTION: TERMINAL REDUCTASE DURING ANAEROBIC GROWTH ON
CC VARIOUS SULFOXIDE AND N-OXIDE COMPOUNDS.
CC -1- CATALYTIC ACTIVITY: REDUCES VARIOUS N-OXIDE AND SULFOXIDE
CC COMPOUNDS INCLUDING TRIMETHYLAMINE N-OXIDE.
CC -1- COFACTOR: MOLYBDENUM (MOLYBDOPTERIN).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Periplasmic.
CC -1- SIMILARITY: BELONGS TO THE PROKARYOTIC MOLYBDOPTERIN-CONTAINING
CC OXIDOREDUCTASE FAMILY.

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CC -----
DR EMBL; U49506; AAD13674.1; -.
DR PDB; 1DMR; 18-MAR-98.
DR PDB; 3DMR; 18-MAR-98.
DR PDB; 4DMR; 18-MAR-98.
DR PDB; 1E18; 11-JUN-00.
DR PDB; 1E5V; 25-AUG-00.
DR PDB; 1E60; 25-AUG-00.
DR PDB; 1E61; 25-AUG-00.
DR InterPro; IPR001467; Molybdopterin.
DR Pfam; PF00384; molybdopterin.1.
DR Pfam; PF01568; Molybdopterin.1.
DR PROSITE; PS00551; MOLYBDOPTERIN_PROK_1; FALSE_NEG.
DR PROSITE; PS00490; MOLYBDOPTERIN_PROK_2; 1.
DR PROSITE; PS00932; MOLYBDOPTERIN_PROK_3; FALSE_NEG.
KW Oxidoreductase; Molybdenum; Periplasmic; Signal; 3D-structure.
FT STGNAL 1 44
FT CHAIN 45 823 DIMETHYL SULFOXIDE REDUCTASE.
FT ACT_SITE 189 189
FT CONFLICT 81 81 T -> S (IN PDB ENTRY).
FT CONFLICT 85 85 E -> A (IN PDB ENTRY).
FT CONFLICT 149 149 Q -> E (IN PDB ENTRY).
FT CONFLICT 276 278 DHV -> EHI (IN PDB ENTRY).
FT CONFLICT 322 322 M -> D (IN PDB ENTRY).
FT CONFLICT 336 337 SD -> EG (IN PDB ENTRY).
FT CONFLICT 337 337 I -> E (IN PDB ENTRY).
FT CONFLICT 354 354 S -> A (IN PDB ENTRY).
FT CONFLICT 416 416 I -> V (IN PDB ENTRY).
FT CONFLICT 498 498 K -> A (IN PDB ENTRY).
FT CONFLICT 568 568 E -> Q (IN PDB ENTRY).
FT CONFLICT 597 597
SQ SEQUENCE 823 AA; 89561 MW; 0E5E901CF2D69273 CRC64;

Query Match 9.3%; Score 81; DB 1; Length 823;
Best Local Similarity 32.8%; Pred. No. 2.8;
Matches 22; Conservative 7; Mismatches 26; Indels 12; Gaps 3;

QY 16 STRDP---CPSPPEVPAPKOCALLEVTPVEVPLNGLTSLSCVACSREPNSILYWG 72
DB 424 ATKPEWELASGASVIVARVMDLEN--PGAEDFDNGTR-----SKFPDYKMAVWG 474
QY 73 NGSPFIEH 79
DB 475 GNPVHH 481

RESULT 5
7LES_DROVI STANDARD; PRT; 2594 AA.
ID 7LES_DROVI
AC P20806;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sevenless protein (EC 2.7.1.112).
GN SEV.
OS Drosophila virilis (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephyroidae; Drosophilidae; Drosophila.
OX NCBI_TaxId=7244;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90319110; PubMed=2115169;
RX Michael W.M., Bowtell D.D.L., Rubin G.M.;

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FT CARBOHYD 1382 1382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1577 1577 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1587 1587 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1587 1587 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1655 1655 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1752 1752 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1776 1776 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1824 1824 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1908 1908 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1966 1966 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 2088 2088 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 2594 AA; 289130 MM; 77DBA356CBAD0BBD CRC64;

Query Match 9.0%; Score 78.5; DB 1; Length 2594;
Best Local Similarity 23.6%; Pred. No. 20;
Matches 30; Conservative 22; Mismatches 44; Indels 31; Gaps 5;

OY 51 TLSTLCVACSRPP-----NFSILYVLGNGSFTEHLPGRLMEGSTRE----- 92
DB 2205 SMSLSDAIDAIALLPOLNMNRLLTLRLTGLSGAF-----GEVYEQGLAEDAEAPQRAIRSL 2259
OY 93 -RGSTGTOLCKALVLEOLTPLALHSTNFSCVL----VDEQVYORHVVLYDLAMAGLRAFL 146
DB 2260 RKGA--SEFAELDLERAOALMSNFKHENIVCLIGICDDTISILIMEHMGAGLLSYLRAAR 2317
OY 147 PPTQDAL 153
DB 2318 PSSQDAL 2324

RESULT 6
MBPL_KIUUA STANDARD; PRT; 754 AA.
AC P3679;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transcription factor MBP1 (MBF subunit P120).
GN MBP1.
OS Kluyveromyces fragilis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93383264; PubMed=8372350;
RA Koch C., Moll T., Neuberg M., Ahorn H., Nasmyth K.;
RT "A role for the transcription factors Mbpl and Swi4 in progression from G1 to S phase.";
RL Science 261:1551-1557(1993).
CC -1- FUNCTION: BINDS TO MCB ELEMENTS (MUL I CELL CYCLE BOX) FOUND IN THE PROMOTER OF MOST DNA SYNTHESIS GENES. TRANSCRIPTIONAL ACTIVATION BY MBF HAS AN IMPORTANT ROLE IN THE TRANSITION FROM G1 TO S PHASE. IT MAY HAVE A DUAL ROLE IN THAT IT BEHAVES AS AN ACTIVATOR OF TRANSCRIPTION AT THE G1-S BOUNDARY AND AS A REPRESSOR DURING OTHER STAGES OF THE CELL CYCLE.
CC -1- SUBUNIT: MBF CONTAINS SWI6 AND MBP1.
CC -1- SUBCELLULAR LOCATION: Nucleus.
CC -1- SIMILARITY: CONTAINS 2 ANK REPEATS.
CC -----
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CC -----
DR EMBL: X74159; CAA52272.1; -.
DR PIR: S37403; S37403.
DR HSSP: P39678; IBM8.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR003163; Yeast_DNA_bind.

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DR EMBL: AF096769; AAD51381.1; JOINED.
DR EMBL: AF096770; AAD51381.1; JOINED.
DR EMBL: X90870; CA62378.1; -.
DR HSSP: P56276; ITLK.
DR MIM: 600922; -.
DR InterPro: IPR001719; Euk_pkinase.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003962; FNIII_repeat.
DR InterPro: IPR003006; I9_MHC.
DR InterPro: IPR003598; I9_C2.
DR InterPro: IPR003600; I9_1like.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00041; fn3; 1.
DR Pfam: PF00047; I9; 8.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00014; FNTYPEIII.
DR SMART: SM00060; FN3; 1.
DR SMART: SM00410; IG_1like; 1.
DR SMART: SM00408; IGC2; 8.
DR SMART: SM00220; S_1Tc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
KW Transferrase; Serine/threonine-protein kinase; Calmodulin-binding;
KW ATP-binding; Phosphorylation; Immunoglobulin domain; Repeat;
KW Alternative Initiation; Alternative splicing.
FT CHAIN 1 1914
FT MYOSIN LIGHT CHAIN KINASE, NON-MUSCLE
FT ISOZYME.
FT MYOSIN LIGHT CHAIN KINASE, SMOOTH-MUSCLE
FT ISOZYME.
FT CHAIN 1914 1914
FT TELOKIN.
FT FOR MYOSIN LIGHT CHAIN KINASE, SMOOTH-
FT MUSCLE ISOZYME.
FT FIBRONECTIN TYPE-III.
FT FOR TELOKIN.
FT PROTEIN KINASE.
FT CALMODULIN-BINDING.
FT IG-LIKE C2-TYPE DOMAIN.
FT ATP (BY SIMILARITY).
FT ATP (BY SIMILARITY).
FT BY SIMILARITY.
FT POLY-GLU.
FT 5 X 28 AA APPROXIMATE TANDEM REPEATS.
FT I-1.
FT I-2.
FT I-3.
FT I-4.
FT I-5 (INCOMPLETE).
FT 6 X 12 AA APPROXIMATE TANDEM REPEATS.
FT II-1 (INCOMPLETE).
FT II-2.
FT II-3.
FT II-4.
FT II-5.
FT II-6.
FT VSGIPKRVANFLEGTPTVRQEGSEIYEDAGSHYLCLKA
FT RTDSGYSTASNAQGVSCSWTLQYVER -> G (IN
FT ISOFORM 2 AND ISOFORM 3B).
FT DEVEYSD -> MKWRQOT (IN ISOFORM 3A,
FT ISOFORM 3B AND ISOFORM 4).
FT GKGQVETLVEKTRKVAQKQEPKAYSAKKEKNIROELISM
FT NCLHHPKLVQCVDAFEERANIVMLEIYSGGEL -> L
FT (IN ISOFORM 4).
FT MISSING (IN ISOFORM 3A AND ISOFORM 3B).
FT MISSING (IN ISOFORM DEL-1790).
FT V -> M (IN REF. 5).
FT S -> P (IN REF. 3).
FT P -> A (IN REF. 3).
FT KPM -> EAH (IN REF. 5).
FT P -> L (IN REF. 3).
FT AAD15922 AND
FT AAD15923).
FT L -> P (IN REF. 5).
FT E -> D (IN REF. 3); AAD15922 AND

FT CONFLICT 1284 1284 AAD15923).
FT M -> I (IN REF. 3; AAD15922, AAD15923 AND
FT AAD15924).
FT CONFLICT 1300 1300 A -> G (IN REF. 5).
FT CONFLICT 1316 1316 L -> S (IN REF. 5).
FT CONFLICT 1326 1326 T -> S (IN REF. 5).
FT CONFLICT 1478 1478 V -> C (IN REF. 5).
FT CONFLICT 1511 1511 S -> T (IN REF. 5); AAD15922 AND
FT AAD15923).
FT CONFLICT 1563 1563 I -> T (IN REF. 5).
FT CONFLICT 1609 1609 A -> P (IN REF. 5).
FT CONFLICT 1639 1639 G -> R (IN REF. 5).
FT CONFLICT 1639 1640 GT -> D (IN REF. 3; AAD15922, AAD15923
Query Match 8.8%; Score 76.5; DB 1; Length 1914;
Best Local Similarity 18.4%; Pred. No. 22;
Matches 48; Conservative 23; Mismatches 72; Indels 117; Gaps 9;
OY 1 TPVSQTTTAA-----TASVSTKPCPSQPPVFAAK----- 32
DB 335 TEVLQKTSSTIRLQAAQVQPEPRAPGLVLSGGEKKRPAPRPATPTPTQPGLSQDV 394
OY 33 -----QCPALEVTPEVEYVPLNGTSLSCVACSRFPNFSILYWLGNCS 75
DB 395 VKKANRRITPMQGRDAPFPKESKPOSOEVENOTVFRK- EVSGTPKEVAM----- 447
OY 76 FIEHLPGRLMEGSTS--RERGS-----TGTOCLKA-----L 104
DB 448 FLEGTPVRQEGSEIYEDAGSHYLCLKAPTRDSQTSCTASNAQGVSCSWTLQYVERL 507
OY 105 VLEQLPALHSTNFCVLYDPEQVYQRRHVVLAQLMAGLRATLP----- 148
DB 508 AVMEVAPSPSSVLKCAVLEGDFV-----LQCSVGRTPVPRITMLNGQPIQYARS 559
OY 149 -----TQALPSSHSS 159
DB 560 TCEAGVAEHLIDALPEDHGT 580
RESULT 8
ID CCR5_RAT STANDARD: PRT: 374 AA.
AC CCR5_RAT
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE C-X-C chemokine receptor type 5 (CXCR-5) (Burkitt's lymphoma
DE receptor 1 homolog) (Neurolymphatic receptor) (NLR).
GN BRLT OR CXCR5
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen; PubMed=8386678;
RX MEDLINE=93238948; Kouda M., Vanetti M., Wang X., Schaefer M., Hoelle V.;
RA "Cloning of a novel putative G-protein-coupled receptor (NLR) which
RT is expressed in neuronal and lymphatic tissue.";
RL FEBS Lett. 321:173-178(1993).
CC -I- FUNCTION: CYTOKINE RECEPTOR THAT BINDS TO B LYMPHOCYTE
CC -I- CHEMOKINE RECEPTOR (BLC) (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- TISSUE SPECIFICITY: EXPRESSED IN NEURONAL AND LYMPHATIC TISSUE.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC
DR      EMBL, X71463; CAA50582.1; -.
DR      PIR, S32785; S32785.
DR      GCRdb; GCR_0648; -.
DR      InterPro: IPR000276; GPCR_Rhodopsn.
DR      Pfam: PF00001; 7tm_1; 1.
DR      PRINTS; PR00237; GPCRRHODOPSN.
DR      PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR      PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW      G-protein coupled receptor; Transmembrane; Glycoprotein; B-cell.
FT      DOMAIN 1 57 EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM 58 78 1 (POTENTIAL).
FT      DOMAIN 79 90 CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM 91 111 2 (POTENTIAL).
FT      DOMAIN 112 126 EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM 127 147 3 (POTENTIAL).
FT      DOMAIN 148 169 CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM 170 190 4 (POTENTIAL).
FT      DOMAIN 191 221 EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM 222 242 5 (POTENTIAL).
FT      DOMAIN 243 261 CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM 262 282 6 (POTENTIAL).
FT      DOMAIN 283 306 EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM 307 327 7 (POTENTIAL).
FT      DOMAIN 328 374 CYTOPLASMIC (POTENTIAL).
FT      CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      DISULFID 124 204 POTENTIAL.
SQ      SEQUENCE 374 AA; 42012 MW; D87A3AC816207319 CRC64;

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Query Match	8.7%;	Score 76;	DB 1;	Length 374;
Best Local Similarity	18.8%;	Pred. No. 3.4;		
Matches	44;	Conservative	33;	Mismatches 61;
				Indels 96;
				Gaps 11.

```

QY      1 TPVQSQTAAAT-----ASVSTSDPCSPGPPVPAKQKCALVTWPEVPLNGT 51
      2 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      3 SPISLDMGATITYNMDDLKELAIYNSNTEIRPLDSDIFCSIEEGPLL-TSKRTIMPV- 58
      4 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      5 LSLSCVACSRPNPSILYIWLG-----NGSFIEH-----L 80
      6 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      7 -----ASLIFELGMMGNILVILNHRHRTSRSTEFERFLHNAVDDLVLFIL 106
      8 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      9 PGRIMSGSTREREGSTQLOLKALVLEQLPALHSTNF-----SCVLVD----- 124
      10 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     107 PFAVAEGSVG--WVLGTFLCKTVI-----ALHKINFCYSLILACIADRYLAIYNAV 157
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY     125 ---PEGVQHRHVYLAQIM-AGLRATLRP-----IQEALPRSHSPQOO 163
      12 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     158 HAYRRRLRLSHITCSFTIMLAGLEALPELLFAKLVQPPHNNESLPPQIFQOENE 211
      19 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT	9			
ID	CXAA_MOUSE	STANDARD;	PRT;	505 AA.
AC	Q9WU54;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Gap junction alpha-10 protein (Connexin 57). (Cx57).			
GN	GJA10.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=99262620; PubMed=10329667;			
RA	Manthey D., Bukauskas F., Kozak C., Willecke K., Lee C.G.;			
RT	"Molecular cloning and functional expression of the mouse gap junction			
RT	gene connexin-57 in human HeLa cells.";			
RL	J. Biol. Chem. 274:14716-14723(1999).			

CC	-	FUNCTION: ONE GAP JUNCTION CONSISTS OF A CLUSTER OF CLOSELY PACKED
CC		PAIRS OF TRANSMEMBRANE CHANNELS, THE CONNEXONS, THROUGH WHICH
CC		MATERIALS OF LOW MW DIFFUSE FROM ONE CELL TO A NEIGHBORING CELL.
CC	-	SUBUNIT: A CONNEXON IS COMPOSED OF A HEXAMER OF CONNEXINS.
CC	-	SUBCELLULAR LOCATION: Integral membrane protein.
CC	-	TISSUE SPECIFICITY: LOW LEVELS WERE DETECTED IN SKIN, HEART,
CC		KIDNEY, TESTIS, OVARY, INTESTINE. EXPRESSION NOT DETECTED IN
CC		BRAIN, SOCRATIC NERVE OR LIVER.
CC	-	SIMILARITY: BELONGS TO THE CONNEXIN FAMILY. ALPHA-TYPE (GROUP II)
CC		SUBFAMILY.
CC		-----
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CC		-----
DR		EMBL; AJ010741; CAB40358.1; -
DR		MGD; MGI:1339969; Gta10.
DR		InterPro: IPR000500; Connexin.
DR		Pfam; PF000029; connexin, 1.
DR		PRINTS; PR00206; CONNEXIN.
DR		SMART; SM00037; CNX; 1.
DR		PROSITE; PS00407; CONNEXINS_1; FALSE_NEG.
DR		PROSITE; PS00408; CONNEXINS_2; 1.
KW		Gap junction; Transmembrane.
FT	DOMAIN	1 19 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	20 40 POTENTIAL.
FT	DOMAIN	41 76 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	77 97 POTENTIAL.
FT	DOMAIN	98 165 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	166 186 POTENTIAL.
FT	DOMAIN	187 209 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	210 230 POTENTIAL.
FT	DOMAIN	231 505 CYTOPLASMIC (POTENTIAL).
FT	SEQUENCE	505 AA; 57115 MW; 77EB9575FD0A274A CRC64;

Query Match 8.7%; Score 75.5; DB 1; Length 505;

Best Local Similarity 23.4%; Pred. No. 5.5;
Matches 29; Conservative 15; Mismatches 39; Indels 41; Gaps 5;

QY	15	RSIDPCPSQPPVPPAPAKQCPALEVTMPVEVPLNGLSL	-----	SCVACSRFPNFSILY	70
Db	188	KCTAPCPNSVDCF	-----	VSRLPTKTFEMFMHSIAISLILILEIFH	232
QY	71	LGNSTFIEHLPRLMEGSTRENGSTGTOLCKALVLEQLPALHSTNF	-----	CVLVD	124
Db	233	LGIKRIINALDGKSSSGTNETNG	-----	PPHSTYISGTQOCWCCSL	276

Qy	125	PEQV	128
		::	
Db	277	PERI	280

RESULT	10
MOZ_HUMAN	
ID_M0Z_HUMAN	STANDARD; PRT, 2004 AA.
AC	Q92794;
DT	15-JUL-1998 (Rel. 36, Created)
DT	15-JUL-1998 (Rel. 36, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Monocytic leukemia zinc finger protein (zinc finger protein 220),
GN	ZNF220 OR MOZ.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
XX	MEDLINE=96376968; PubMed=8782817;

RA Borrow J., Stanton V.P. Jr., Andresen J.M., Becher R., Behm F.G.,
RA Chaganti R.S.K., Clavin C.I., Distche C., Dube I., Erischauf A.M.,
RA Hosman D., Mtelman F., Volinia S., Watmore A.E., Hosman D.E.;
RT "The translocation t(8;16)(p11;p13) of acute myeloid leukaemia fuses
RT a putative acetyltransferase to the CREB-binding protein.";
RL Nat. Genet. 14:33-41(1996).
CC -1- FUNCTION: MAY REPRESENT A CHROMATIN-ASSOCIATED ACETYLTRANSFERASE.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DISEASE: PARTICIPATES IN A T(8;16)(p11;p13) CHROMOSOMAL
CC TRANSLOCATION THAT PRODUCES A MOZ-CBP CHIMERA OBSERVED IN THE
CC M4/M5 SUBTYPE OF ACUTE MYELOID LEUKEMIA.
CC -1- SIMILARITY: CONTAINS 2 PHD-TYPE ZINC FINGERS.
CC -1- SIMILARITY: BELONGS TO THE MYST (SAS/MOZ) FAMILY.
CC -----
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CC -----
DR EMBL; U47742; AAC50662.1; -
DR HSSP; 060631; 4GBQ.
DR MIM; 601408; -
DR InterPro; IPR001386; linker_histone.
DR InterPro; IPR002717; MOZ_SAS.
DR InterPro; IPR001965; PHD.
DR Pfam; PF01853; MOZ_SAS; 1.
DR Pfam; PF00628; PHD; 2.
DR SMART; SM00526; H15; 1.
DR SMART; SM00249; PHD; 2.
KW Proto-oncogene; Chromosomal translocation; Zinc-finger; Repeat;
KW Nuclear protein.
FT ZN_FING 206 256 PHD-TYPE 1.
FT ZN_FING 259 313 PHD-TYPE 2.
FT DOMAIN 371 379 POLY-SER.
FT ZN_FING 538 560 POLY-SER.
FT DOMAIN 788 801 POLY-TYR.
FT DOMAIN 989 995 POLY-GLU.
FT DOMAIN 1019 1026 POLY-ARG.
FT DOMAIN 1069 1078 POLY-GLU.
FT DOMAIN 1147 1150 POLY-GLU.
FT DOMAIN 1221 1242 GLU-RICH.
FT DOMAIN 1267 1302 GLU-RICH.
FT DOMAIN 1411 1414 POLY-GLU.
FT DOMAIN 1593 1597 POLY-SER.
FT DOMAIN 1643 1704 GLN/PRO-RICH.
FT DOMAIN 1897 1977 MET-RICH.
FT SITE 1546 1547 BREAKPOINT FOR TRANSLOCATION TO FORM
FT MOZ-CBP.
SQ SEQUENCE 2004 AA; 225054 MW; 9FDBAC3792854BA CRC64;

Query Match 8.7%; Score 75.5; DB 1; Length 2004;
Best Local Similarity 24.9%; Pred. No. 29;
Matches 42; Conservative 17; Mismatches 61; Indels 49; Gaps 7;

OY 20 PCPSOPVPEPAKQCPALE-----VTWDEV-EVPLNGTSLSCVACSRPNFSILYW 70
DB 1685 POPQPPPPPPQPPPLSCSMNNSFPAPMIMEIPESGS----- 1725

OY 71 LGNSGFHLGRLEMGSTSRERGSTGTQLCKALVLEOLT-----PAL--H 114
DB 1726 TGNISITIERIPDGCAGSYSP--SNFSLAK-----IQQLTMTIMDPRAMPYSHSPAVSY 1780

OY 115 STNSCVLVDEPQVYVORHIVLAQLAGLRATLPQGLALPSHSSPQOQ 163
DB 1781 ATSVSLSTGLAQLAPSHPLAGTPOAQOATTPPPVPLASTMTNLISPLDQ 1829

RESULT 11
ILIS_RAT

ID ILIS_RAT STANDARD: PRT; 416 AA.
AC P43303;
DT 01-NOV-1995 (Rel. 32; Created)
DT 01-NOV-1995 (Rel. 32; Last sequence update)
DT 01-MAR-2002 (Rel. 41; Last annotation update)
DE Interleukin-1 receptor, type II precursor (IL-1R-2).
GN IL1R2 OR IL1RB OR IL-1R2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Euteleostomi; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95035882; PubMed=7524717;
RA Bristol J., Gatti S., Malinowsky D., Bjork L., Sundgren A.K.,
RA Barfal T.;
RT "Interleukin-1 stimulates the expression of type I and type II
RT interleukin-1 receptors in the rat insulinoma cell line R1m5F;
RT sequencing a rat type II interleukin-1 receptor, cDNA.";
RL Eur. Cytokine Netw. 5:319-330(1994).
CC -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-1 ALPHA (IL-1A), BETA (IL-1B),
CC AND INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN (IL-1RA).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -----
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CC -----
DR EMBL; 222812; CAA80465.1; -
DR HSSP; P14778; IIRB.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR004077; Intlik_receptorII_pre.
DR InterPro; IPR004074; Intlik_receptorII.
DR Pfam; PF00047; Ig; 3.
DR PRINTS; PR01539; INTRLEUKINR2.
DR PRINTS; PR01536; INTRLEUKINR12F.
DR SMART; SM00409; IG; 3.
KW Immunoglobulin domain; Receptor; Glycoprotein; Transmembrane; Signal;
KW Repeat.
FT SIGNAL 1 13 POTENTIAL.
FT CHAIN 14 416 INTERLEUKIN-1 RECEPTOR, TYPE II.
FT DOMAIN 14 355 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 356 381 POTENTIAL.
FT DOMAIN 382 416 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 57 127 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 157 127 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 263 345 IG-LIKE C2-TYPE DOMAIN 3.
FT DISULFD 64 120 BY SIMILARITY.
FT DISULFD 164 219 BY SIMILARITY.
FT DISULFD 270 338 BY SIMILARITY.
FT CARBOHD 124 124 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 208 208 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 416 AA; 46353 MW; 50BFBA48881C5DAE CMC64;

Query Match 8.6%; Score 74.5; DB 1; Length 416;
Best Local Similarity 20.3%; Pred. No. 5.4;
Matches 27; Conservative 21; Mismatches 46; Indels 39; Gaps 4;

OY 66 SILVWLGNGSTLE-HLPGRLMEGSTSRERGSTGTQLCKALVLEOLTLPALHSTNSCYLV 123
DB 282 YIVWMANSTFISVAVPRGRVTEGLIHQYSENDYVVEVSLFDVFKEDLTDKCYAT 341

OY 124 DPEQVYVGRH-----VYLAQQLMAGLR-----ATLPPT 149

Db 342 NPNRFSGLHTTVKEVSTFSMGIALAPLSLIIIVGAIWIRCKROAGKTYGLTKLPTD 401
QY 150 QEALPSSHSFPQ 162
Db 402 NQDFP---SSPNO 411

RESULT 12
MY15_MOUSE STANDARD: PRT: 3511 AA.
ID MY15_MOUSE
AC G90224: 070395; Q9QWU6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myosin XV (unconventional myosin-15).
GN MYO15.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RX MEDLINE=20021762; PubMed=10552926;
RA Liang Y., Wang A., Belyantseva I.A., Anderson D.W., Probst F.J.,
RA Barber T.D., Miller W., Touchman J.W., Jin L., Sullivan S.L.,
RA Sellers J.R., Camper S.A., Lloyd R.V., Kachar B., Friedman T.B.,
RA Fridell R.A.;
RT "Characterization of the human and mouse unconventional myosin XV
RT genes responsible for hereditary deafness DFNB3 and Shaker 2.";
RL Genomics 61:243-258(1999).
RN [2]
RP SEQUENCE OF 1168-2970 FROM N.A., AND VARIANT SH2 TYR-1779.
RC TISSUE=Embryo;
RX MEDLINE=98267310; PubMed=9603735;
RA Probst F.J., Fridell R.A., Raphael Y., Saunders T.L., Wang A.,
RA Liang Y., Morell R.J., Touchman J.W., Lyons R.H., Noben-Trauth K.,
RA Friedman T.B., Camper S.A.;
RT "Correction of deafness in shaker-2 mice by an unconventional myosin
RT in a BAC transgene.";
RL Science 280:1444-1447(1998).
RN [3]
RP SEQUENCE OF 1237-1823 FROM N.A., AND VARIANT SH2 TYR-1779.
RC STRAIN=C57BL/6;
RX MEDLINE=98369604; PubMed=9703981;
RA Wakabayashi Y., Takahashi Y., Kikkawa Y., Okano H., Mishima Y.,
RA Ushiki T., Yonekawa H., Komihama R.;
RT "A novel type of myosin encoded by the mouse deafness gene shaker-2.";
RL Biochem. Biophys. Res. Commun. 248:655-659(1998).
CC -I- FUNCTION: MYOSINS ARE ACTIN-BASED MOTOR MOLECULES WITH ATPASE
CC ACTIVITY. UNCONVENTIONAL MYOSINS SERVE IN INTRACELLULAR MOVEMENTS.
CC THEIR HIGHLY DIVERGENT TAILS ARE PRESUMED TO BIND TO MEMBRANOUS
CC COMPARTMENTS, WHICH WOULD BE MOVED RELATIVE TO ACTIN FILAMENTS (BY
CC SIMILARITY). MAY PLAY A ROLE IN THE FORMATION OR MAINTENANCE OF
CC THE ACTIN-RICH STRUCTURES OF THE INNER EAR SENSORY HAIR CELLS.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -I- TISSUE SPECIFICITY: IN THE DEVELOPING INNER EAR. EXPRESSED IN
CC COCHLEA AND VESTIBULAR APPARATUS. EXPRESSION APPEARS TO BE
CC RESTRICTED TO COCHLEAR NEUROSENSORY CELLS AND UPPER EPITHELIAL
CC LAYER OF MACULA SACCULE. ALSO EXPRESSED IN MACULA UTRICULI AND
CC CRISTAE AMPULLARIS OF THE SEMICIRCULAR CANALS. IN ADULT COCHLEAR
CC HAIR CELLS, HIGHEST EXPRESSION IN STEREOCILIA AND APICAL BODY.
CC -I- DISEASE: DEFECTS IN MYO15 ARE THE CAUSE OF SHAKER 2 (SH2), A
CC CONDITION CAUSING DEAFNESS, CIRCLING BEHAVIOR, HEADTOSING AND
CC HYPERACTIVITY. AUDITORY HAIR CELLS OF AFFECTED ANIMALS HAVE VERY
CC SHORT STEREOCILIA AND A LONG ACTIN-CONTAINING PROTRUSION AT THEIR
CC BASAL END.
CC -I- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
CC -I- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
CC -I- SIMILARITY: CONTAINS 2 IO DOMAINS.
CC -I- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -----
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CC -----

DR EMBL: AF144095; AAF05904.1; -;
DR EMBL: AF053130; AAC40124.1; -;
DR EMBL: AB014510; BAB36582.1; -;
DR HSSP: P08799; ILVK.
DR MGD: MGI:1261811; Myo15.
DR InterPro: IPR000299; Band_4.1.
DR InterPro: IPR000048; IO.
DR InterPro: IPR000857; MYTH4.
DR InterPro: IPR001452; MYTH3.
DR InterPro: IPR001609; myosin_head.
DR Pfam: PF00612; IO; 2.
DR Pfam: PF00063; myosin_head; 1.
DR Pfam: PF00784; MYTH4; 2.
DR PRINTS: PR00193; MYOSINHEAVY.
DR ProDom: PD000355; myosin_head; 1.
DR SMART: SM00015; IO; 2.
DR SMART: SM00242; MYSC; 1.
DR SMART: SM00139; MYTH4; 2.
DR SMART: SM00326; SH3; 1.
DR PROSITE: PS50096; IO; 2.
DR PROSITE: PS50002; SH3; 1.
DR PROSITE: PS00660; BAND_4_1; FALSE_NEG.
DR PROSITE: PS00661; BAND_4_1_2; FALSE_NEG.
DR PROSITE: PS50057; BAND_4_1_3; FALSE_NEG.
DR MYOSIN: ATP-binding; Actin-binding; Coiled coil; Repeat; SH3 domain;
KW Disease mutation; Deafness.
FT DOMAIN 1 1871
FT 1872 2013 HEAD OR MOTOR DOMAIN.
FT DOMAIN 2014 3511 NECK OR REGULATOR DOMAIN.
FT DOMAIN 1307 1334 TAIL.
FT DOMAIN 1776 1783 COILED COIL (POTENTIAL).
FT DOMAIN 1886 1908 ACTIN-BINDING (POTENTIAL).
FT DOMAIN 1909 1938 IO 1.
FT DOMAIN 2848 2934 IO 2.
FT DOMAIN 3187 3424 SH3.
FT NP_BIND 1299 1306 BAND 4.1-LIKE.
FT VARIANT 1779 1779 ATP (POTENTIAL).
FT CONFLICT 1330 1331 C -> Y (IN SH2).
FT CONFLICT 1579 1579 MISSING (IN REF. 2).
FT CONFLICT 1955 1972 L -> R (IN REF. 3).
FT CONFLICT 2077 2077 MISSING (IN REF. 2).
FT CONFLICT 2139 2139 L -> M (IN REF. 2).
FT CONFLICT 2953 2953 L -> P (IN REF. 2).
FT CONFLICT 2953 2953 V -> A (IN REF. 2).
SQ SEQUENCE 3511 AA; 395533 MW; 38C962F98A2D395B CMC64;

Query Match 8.6%; Score 74.5; DB 1; Length 3511;
Best Local Similarity 24.3%; Pred. No. 73;
Matches 45; Conservative 24; Mismatches 67; Indels 49; Gaps 9;

QY 9 AATAVRSTDPDPPSQ---PVPPAAK--QCPLAEVTPVEVPPLNLTLSLCV-----A 58
Db 2010 AAVRAAPRLQAPCVTLPLDINNYPMAKFTIRCKEKSFGMLTVPLKMLTRLPLPEHHAAE 2069
QY 59 CSRPPEPSILYWGNN-----GSFTEH-----LPRLWE--GSTS 90
Db 2070 ISYFK--LILRFMGDHLHGTQEMILGNIVHOGVLEPAIRDELIAQLAQNVRNPAVN 2127
QY 91 RERGSTGTQCALVEQLTPALHSTNFCVLDP-----QVYORHVVLAQLMAGIRAT 145
Db 2128 SKRG-----WLLAACLSGFAPSPDLKFLKLFVSDYGONGFQAVCOHRLQLAMGSGAART 2183
QY 146 LPPTQ 150
Db 2184 FPPTQ 2188

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RESULT 13
ALCL_HUMAN STANDARD: PRT; 353 AA.
AC P01876;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig alpha-1 chain C region.
GN IGHAI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=84130179; PubMed=6421489;
RA Flanagan J.G., Lefranc M.-P., Rabbits T.H.;
RT "Mechanisms of divergence and convergence of the human immunoglobulin
RT alpha 1 and alpha 2 constant region gene sequences.";
RL Cell 36:681-688(1984).
RN [2]
RP SEQUENCE (MYELOMA PROTEIN BUR), AND DISULFIDE BONDS.
RA MEDLINE=79151016; PubMed=107164;
RA Putnam F.W., Liu Y.-S.V., Low T.L.K.;
RT "Primary structure of a human IgM immunoglobulin. IV. Streptococcal
RT IgM protease, digestion, Fab and Fc fragments, and the complete
RT amino acid sequence of the alpha 1 heavy chain.";
RL J. Biol. Chem. 254:2865-2874(1979).
RN [3]
RP SEQUENCE (MYELOMA PROTEIN TRO).
RA MEDLINE=76023781; PubMed=809311;
RA Kretzlin H., Altevoigt P., Ruban E., Kortt A., Starosck K.,
RA Hilschmann N.;
RT "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.),
RT I. The amino acid sequence of the H-chain, alpha-type, subgroup III;
RT structure of the complete IgA-molecule.";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
RN [4]
RP DISULFIDE BONDS.
RA MEDLINE=80114124; PubMed=393607;
RA Yang C.-Y., Kretzlin H., Goltz H., Hilschmann N.;
RT "Rule of antibody structure. Primary structure of a human monoclonal
RT IgA-immunoglobulin (myeloma protein Tro). VII. Purification and
RT characterization of the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 360:1919-1940(1979).
RN [5]
RP REVIEW.
RX MEDLINE=91054387; PubMed=2241915;
RA Kerr M.A.;
RT "The structure and function of human IgA.";
RL Biochem. J. 271:285-296(1990).
CC -I- FUNCTION: IG ALPHA IS THE MAJOR IMMUNOGLOBULIN CLASS IN BODY
CC SECRETIONS. IT MAY SERVE BOTH TO DEFEND AGAINST LOCAL INFECTION
CC AND TO PREVENT ACCESS OF FOREIGN ANTIGENS TO THE GENERAL
CC IMMUNOLOGIC SYSTEM.
CC -I- SUBUNIT: MONOMERIC OR POLYMERIC.
CC -----
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CC -----
DR EMBL; J00220; AAC82528.1; ALT_INIT.
DR PIR; A02171; AIHU.
DR PIR; A23360; A23360.
DR HSP; P01810; 2PBJ.
DR MIM; 146900; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig-cl.
DR Pfam; PF00047; Ig_3.

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DR SMART; SM00407; IGcl. 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 26 85
FT DISULFID 77 101 INTERCHAIN (WITH HEAVY CHAIN).
FT DISULFID 122 122 OR 123-182 (IN REF. 4).
FT DISULFID 123 180 INTERCHAIN (WITH HEAVY CHAIN) (OR 180, IN
FT DISULFID 147 204 REF. 4).
FT DISULFID 182 182 INTERSUBUNIT BOND (PROBABLE).
FT DISULFID 192 192 WITH J CHAIN.
FT DISULFID 250 313 O-LINKED.
FT DISULFID 352 352 O-LINKED.
FT CARBOHYD 105 105 O-LINKED.
FT CARBOHYD 111 111 O-LINKED.
FT CARBOHYD 113 113 O-LINKED.
FT CARBOHYD 119 119 O-LINKED.
FT CARBOHYD 121 121 O-LINKED.
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .).
FT CARBOHYD 340 340 N-LINKED (GLCNAC. . .).
FT CONFLICT 163 165 TPS -> PST (IN REF. 2).
FT CONFLICT 176 176 E -> B (IN REF. 3).
FT CONFLICT 190 190 P -> S (IN REF. 3).
FT CONFLICT 227 227 R -> H (IN REF. 3).
FT CONFLICT 231 231 H -> R (IN REF. 3).
FT CONFLICT 290 290 T -> E (IN REF. 3).
SQ SEQUENCE 353 AA; 37654 MW; EBALL1BCB7E85DB21 CRC64;

Query Match 8.4%; Score 73.5; DB 1; Length 353;
Best Local Similarity 24.2%; Pred. No. 5.6;
Matches 40; Conservative 17; Mismatches 81; Indels 27; Gaps 8;

OY 1 TPVSOTTAATASVSTDCPCSPVPFPAKQC-PALEVTPEVEVPLNGT-LSISGVA 58
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 91 TNPQDVTVPVPCVSTPTPTPTPTPTPTPT-PSPCCHPLRLSLHNPALDLGSEANLTC- 148
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 59 CSRPNFSILWLGNGSFTEHLPGRLWEGSTSR--RSGTGTQALCALVLEQTPAL--- 113
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 149 -----LTLGRDASGVTF---TWTPSSGKSAVQGPEDRLGCVSVSLPGCAEP 195
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 114 --HSTNFCVVLDPDQVQVGRHVLNQLNAGLRA---TLPPQDAL 153
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 196 WNHGKFTCTAAYPESKTPPLATFLSKSGNTERFVHLPLPPEEL 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 14
TSP2_MOUSE STANDARD: PRT; 1172 AA.
AC Q03350;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Thrombospondin 2 precursor.
GN THBS2 OR TSP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10990;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92147683; PubMed=1371115;
RA Laherty C.D., O'Rourke K., Wolf F.W., Katz R., Seidlin M.F.,
RA Dixit V.M.;
RT "Characterization of mouse thrombospondin 2 sequence and expression
RT during cell growth and development.";
RL J. Biol. Chem. 267:3274-3281(1992).
RN [2]
RP SEQUENCE OF 1-873 FROM N.A.
RX MEDLINE=91302287; PubMed=1712771;
RA Bornstein P., O'Rourke K., Wikstrom K., Wolf F.W., Katz R., Li P.,

```

Query Match	Best Local Similarity	8.4%,	Score 73.5:	DB 1:	Length 1172:			
Matches	35;	Conservative	17;	Mismatches	54;	Indels	37;	Gaps
QY	1	TPVSTGTTAATGASVSTRKDPCPSQPPVPAKQCPALEVTWTFV---	EVPLNGTSLSSC	56				
Db	501	SPMSACTYTCAGGILRERSVRCNSPEPQY-GGKDCYG-DYTEHQMKNKNSCPIDGCLSNRC	558					
QY	57	--VACSNFNPNSILYW-----LGNSFIEHLPGRLWGSTSRKSGTGTOLCKAL	104					
Db	559	FPGAKCNSEFPDGS---WCGSGCPVGFGLNGTGHCELD-----DECAYVTIDICFS-	603					
QY	105	VLEQUTPALHSTN--FSCVLYDP	125					
Db	604	--TNKAPRCVNTNPGFHLPCPP	624					
RESULT 15								
LHR_ECOLI	ID	LHR_ECOLI	STANDARD;	PRT;	1538	AA.		
AC	P30015;							
DT	01-APR-1993 (Rel. 25, Created)							
DT	01-JUN-1994 (Rel. 29, Last sequence update)							
DT	16-OCT-2001 (Rel. 40, Last annotation update)							
DE	Probable ATP-dependent helicase Ihr (Ec 3.6.1.-) (Large helicase-related protein).							
DE	LHR OR RHLF OR B1653.							
OS	Escherichia coli.							
OC	Bacteria: Proteobacteria; gamma subdivision: Enterobacteriaceae;							
OC	Escherichia.							
OX	NCBI_TaxID=562;							
RN	[1]							
RP	SEQUENCE FROM N.A.							
RC	STRAIN-K12;							
RX	MEDLINE=9603370; PubMed=7559321;							
RA	Reuven N.B., Koonin E.V., Rudd K.E., Deutscher M.P.;							
RT	"The gene for the longest known Escherichia coli protein is a member of helicase superfamily II."							
RL	J. Bacteriol. 177:5393-5400(1995).							
RN	[2]							
RP	SEQUENCE FROM N.A.							
RC	STRAIN-K12 / MGI655;							
RX	MEDLINE=97426617; PubMed=9278503;							
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,							
RT	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,							
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,							
RT	Mau B., Shao Y.;							
RL	"The complete genome sequence of Escherichia coli K-12.";							
RN	Science 277:1453-1474(1997).							
RP	[3]							
RC	SEQUENCE FROM N.A.							
RX	STRAIN-K12;							
RA	MEDLINE=97251357; PubMed=9097039;							
RA	Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,							
RT	Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,							
RA	Kitagawa M., Maeno K., Miki T., Mizobuchi K., Mori H., Mori T.,							

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OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 21:46:44 ; Search time 1828.01 Seconds
(without alignments)
5632.276 Million cell updates/sec

Title: US-09-786-130-32

Perfect score: 492

Sequence: 1 acaccgtctcgcagaccac.....gcagtcacagcagcaggt 492

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_ov:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
------------	-------	-------------	--------	----	-------------

1	492	100.0	492	6	E58835	E58835 Interleukin
2	492	100.0	585	6	AB019504	AB019504 Homo sapi
3	492	100.0	744	6	E58840	E58840 Interleukin
4	492	100.0	1348	6	AX005900	AX005900 Sequence
5	492	100.0	1348	9	AF110799	AF110799 Homo sapi
6	492	100.0	1355	9	AF1122906	AF1122906 Homo sapi
7	418.2	85.0	7063	6	AF110801	AF110801 Homo sapi
8	418.2	85.0	7063	6	AX005904	AX005904 Sequence
9	411	83.5	411	6	E58837	E58837 Interleukin
10	290.6	59.1	1360	6	AX005906	AX005906 Sequence
11	290.6	59.1	1726	9	AF215907	AF215907 Homo sapi
12	277.8	56.5	626	10	AF154569	AF154569 Rattus no
13	272.2	55.3	873	10	AF110803	AF110803 Mus muscu
14	272.2	55.3	1310	10	BC018332	BC018332 Mus muscu
15	270.6	55.0	1422	10	AF122907	AF122907 Mus muscu
16	269	54.7	405	6	E58836	E58836 Interleukin
17	269	54.7	582	10	AB019505	AB019505 Mus muscu
18	269	54.7	847	6	E58844	E58844 Interleukin
19	251.6	51.1	2612	10	AF110802	AF110802 Mus muscu
20	235.2	47.8	351	6	E58841	E58841 Interleukin
21	187.6	38.1	2528	9	AF122908	AF122908 Homo sapi
22	187.6	38.1	7832	6	AX005908	AX005908 Sequence
23	187.6	38.1	8232	9	AF110798	AF110798 Homo sapi
24	187.6	38.1	191986	9	AP002490	AP002490 Homo sapi
25	187.6	38.1	196424	9	AP000719	AP000719 Homo sapi
26	145	29.5	1038	6	AX005902	AX005902 Sequence
27	145	29.5	1038	9	AF110800	AF110800 Homo sapi
28	141	28.7	2234	6	E58839	E58839 Interleukin
29	105.6	21.5	228133	2	AC098723	AC098723 Mus muscu
30	94.6	19.2	88166	2	AC097860	AC097860 Rattus no
31	70.8	14.4	657	14	MC0271163	AJ271163 Molluscum
32	67.6	13.7	190289	14	MC060315	U60315 Molluscum
33	57	11.6	216	6	E58838	E58838 Interleukin
34	52.2	10.6	253	6	E58843	E58843 Interleukin
35	47.4	9.6	125020	9	AF429315	AF429315 Homo sapi
36	46.6	9.5	125020	9	AF429315	AF429315 Homo sapi
37	41.6	8.5	4612	1	AF317284	AF317284 Burkholde
38	41.2	8.4	38734	1	SC10A5	AL021529 Streptomy
39	41.2	8.4	40352	2	SC061A	AL356595 Streptomy
40	41.2	8.4	165253	2	OS0N00048	AL606615 Oryza sat
41	41	8.3	2636	9	BC013947	BC013947 Homo sapi
42	41	8.3	4283	9	AB020648	AB020648 Homo sapi
43	40.4	8.2	582	10	AB060081	AB060081 Mus muscu
44	39.2	8.0	225506	2	AC102953	AC102953 Homo sapi
45	39	7.9	83039	9	AL137074	AL137074 Human DNA

ALIGNMENTS

RESULT	1	492 bp	DNA	linear	PAT	31-JAN-2002
LOCUS	E58835	Interleukin 18 binding protein.				
DEFINITION	E58835	Interleukin 18 binding protein.				
ACCESSION	E58835.1	GI:18629908				
VERSION	JP 2000210087-A/1.					
KEYWORDS						
SOURCE	Homo sapiens					
ORGANISM	Homo sapiens					
REFERENCE						
AUTHORS	Torikoshi, K., Tanai, M. and Kurimoto, M.					
TITLE	Interleukin 18 binding protein					
JOURNAL	Patent: JP 2000210087-A 1 02-AUG-2000;					
COMMENT	HAYASHIBARA BIOCHEM LAB INC					
OS	Homo sapiens (human)					
PN	JP 2000210087-A/1					
PD	02-AUG-2000					
PF	28-MAY-1999 JP 1999149498					
PI	RAKUJI TORIKOSHI, MADOKA TANAI, MASASHI KURIMOTO PC					
	C12N15/09,A61K31/00,A61K38/00,A61K39/395,C07K14/47,C07K14/715, PC					

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007K16/18//
PC C12P21/08,C12N15/00,A61K37/02
CC
CC Key Location/Qualifiers
FH mat_peptide (1)..(492).
FEATURES
    source 1..492
            Location/Qualifiers
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
BASE COUNT 97 a 171 c 136 g 88 t
ORIGIN

Query Match 100.0%: Score 492; DB 6; Length 492;
Best Local Similarity 100.0%: Pred. No. 3.2e-102;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acactgtctcgcagaccacacacagctgcactgcctcagttagaagcacaagagacccc 60
DB 1 ACACCTGTCTGCAGACCCACACAGCTGCCTGCTCAGTTAGAAAGCAAGAGACCCC 60
QY 61 tgcctcccccagccccagtgctccacagcactaagcagtgctccagcattggaagtacc 120
DB 61 TGCCCTCCACAGCCGCCAGTGTTCACAGCAGCTAAGCAAGTGTCCAGCATTTGGAAAGTGAGCC 120
QY 121 tggcagaggtggaagtgccactgaatgaaagcgtgagcttaacctgtgtgtgcctgcagc 180
DB 121 TGCCAGAGGTGGAAGTGTCCACTGAATGGAAGCGTGAAGCTTAATCCTGTGTGCTGCAAC 180
QY 181 cgtctccccaacttcagactcctcactctgctggtgcgaatggtctcctcattagaacctc 240
DB 181 CGCTTCCCAACTTCAGACTCCTCTACTGTGCTGGGCAATGTTCTTCAATTAGACACCTC 240
QY 241 ccagggcgactgtggaaggagagacacagccggaacgttggagacagagtaacgagctg 300
DB 241 CCAGGCCGACTGTGGAGGGGAGCACACAGCCGGGAACGTGGAGCACAGGTACGACAGCTG 300
QY 301 tgcgaagccttggtgtcgtgaagagctggaacccctgcccctgcagacagacaacttcctgt 360
DB 301 TGCAAGGCTTGTGTCTGTGAGAGAGCTGACCTTGCCTGCAACAGCACTTCTCTGT 360
QY 361 gtgtcgtgtgaacccctgaacaggtgttcacagcgttcacgtcgtcctgtgcccagctcgtg 420
DB 361 GTGCTCGTGAACCTTGAAACAGGTGTCCAGCGTCAAGTGTCTGTGCCCCAGCTCGGGGT 420
QY 421 gggctggaagggaacctgtgcccccaacccaagaagaccctgcctccagccacagagctcca 480
DB 421 GGGCTGAAGGGCAACCTTGCCTCCACCCACCAAGAGCCCTGCCCTCCAGCCACAGCAGTCCA 480
QY 481 cagcagcagaggt 492
DB 481 CAGCAGCAGGGT 492

RESULT 2
ABO19504 585 bp mRNA linear PRI 31-MAR-1999
LOCUS Homo sapiens mRNA for interleukin-18 binding protein, complete cds.
DEFINITION ABO19504
VERSION ABO19504.1 GI:4586394
KEYWORDS interleukin-18 binding protein.
SOURCE Homo sapiens (isolate:white) male liver cdna to mRNA.
ORGANISM Homo sapiens
Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (sites)
Alizawa,Y., Akita,K., Tanai,M., Korigoe,K., Mori,T., Nishida,Y.,
Ushio,S., Nukada,Y., Tanimoto,T., Ikegami,H., Ikeda,M. and
Kurimoto,M.
TITLE Cloning and expression of interleukin-18 binding protein
JOURNAL FEBS Lett. 445 (2-3), 338-342 (1999)
MEDLINE 99192308
REFERENCE 2 (bases 1 to 585)
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AUTHORS Alizawa,Y.
TITLE Direct Submission
JOURNAL Submitted (04-NOV-1998) Yasushi Alizawa, Hayashibara Biochemical
Laboratories, Inc., Fujisaki Institute; 675-1, Fujisaki, Okayama,
Okayama 702-8006, Japan (E-mail:fujisaki@hayashibara.co.jp,
Tel:81-86-276-3141, Fax:81-86-276-6885)
COMMENT Sequence updated (30-Nov-1998).
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LOCUS E58840 744 bp DNA linear PAT 31-JAN-2002
DEFINITION Interleukin 18 binding protein.
ACCESSION E58840
VERSION E58840.1 GI:18629913
KEYWORDS JP 2000210087-A/6.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 744)
AUTHORS Torikoshi, K., Tanai, M. and Kurimoto, M.
TITLE Interleukin 18 binding protein
JOURNAL Patent: JP 2000210087-A 6 02-AUG-2000;
HAYASHIBARA BIOCHEM LAB INC
COMMENT OS Homo sapiens (human)
PN JP 2000210087-A/6
PD 02-AUG-2000
PE 28-MAY-1999 JP 1999149498
PR
PI RAKUJI TORIKOSHI, MADOKA TANAI, MASASHI KURIMOTO
C12N15/09,A61K31/00,A61K38/00,A61K39/395,C07K14/47,C07K14/715, PC
C07K16/18//
PC C12P21/08,C12N15/00,A61K37/02
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DB 520 GTGTCTGTGTGACCTGAACAGGTGTGTCAGGCTGACAGTGTCTGTGCTGTGGCT 579
QY 421 gggcttgaagggcaaccttgcaccacccaagaagccctgcctccagacacagcaatcca 480
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QY 481 cagcagcagaggt 492
DB 640 CAGCAGCAGAGGT 651

RESULT 4
LOCUS AX005900 1348 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 1 from Patent WO9909063.
ACCESSION AX005900
VERSION AX005900.1 GI:9928886
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1348)
AUTHORS Rubinstein, M. and Kim, S.H.
TITLE Interleukin-18 binding proteins, their preparation and use
JOURNAL Patent: WO 9909063-A 1 25-FEB-1999;
RUBINSTEIN MENACHEM (IL); KIM SOO HYUN (IL)
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QY 481 cagcagcagaggt 492
DB 630 CAGCAGCAGAGGT 641
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LOCUS AF110799 1348 bp mRNA linear PRI 03-MAR-1999
DEFINITION Homo sapiens interleukin-18 binding protein a precursor (IL18BP)
mRNA, complete cds.
ACCESSION AF110799

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VERSION      AF110799.1  GI:4324927
KEYWORDS
SOURCE       human
ORGANISM     Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
              1 (bases 1 to 1348)
              Novick,D., Kim,S.H., Fantuzzi,G., Reznikov,L.L., Dinarello,C.A. and
              Rubinstein,M.
TITLE        Interleukin-18 binding protein: a novel modulator of the Th1
              cytokine response
JOURNAL      Immunity 10 (1), 127-136 (1999)
MEDLINE      99146382
REFERENCE    2 (bases 1 to 1348)
AUTHORS      Novick,D., Kim,S.H., Fantuzzi,G., Reznikov,L.L., Dinarello,C.A.
              and Rubinstein,M.
TITLE        Direct Submission
JOURNAL      Submitted (04-DEC-1998) Molecular Genetics, Weizmann Institute of
              Science, P.O. Box 26, Rehovot 76100, Israel
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DB 630 CAGCAGCAGAGGT 641
RESULT 6
LOCUS       AF122906 1355 bp mRNA linear PRI 28-JUN-1999
DEFINITION Homo sapiens MC51L-53L-54L homolog mRNA, complete cds.
ACCESSION  AF122906
VERSION     AF122906.1 GI:5231015
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE   1 (bases 1 to 1355)
AUTHORS     Xiang,Y. and Moss,B.
TITLE       Identification of human and mouse homologs of the MC51L-53L-54L
             family of secreted glycoproteins encoded by the Mollusum
             contagiosum poxvirus
JOURNAL     Virology 257 (2), 297-302 (1999)
MEDLINE     99263157
PUBMED      10329540
REFERENCE   2 (bases 1 to 1355)
AUTHORS     Xiang,Y. and Moss,B.
TITLE       Direct Submission
JOURNAL     Submitted (25-JAN-1999) NIAID/LVD, NIH, 9000 Rockville Pike,
             Bethesda, MD 20892, USA
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Best Local Similarity 100.0%; Pred. No. 3e-102;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 7

AF110801

LOCUS

3630 bp mRNA linear PRI 03-MAR-1999

DEFINITION

Homo sapiens Interleukin-18 binding protein c precursor (IL18BP)

ACCESSION

AF110801

VERSION

AF110801.1 GI:4324931

KEYWORDS

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SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

TITLE

Novick, D., Kim, S.H., Fantuzzi, G., Reznikov, L.L., Dinarello, C.A. and

JOURNAL

Interleukin-18 binding protein: a novel modulator of the Th1

MEDLINE

cytokine response

REFERENCE

Immunology 10 (1), 127-136 (1999)

AUTHORS

2 (bases 1 to 3630)

JOURNAL

99146382

MEDLINE

Novick, D., Kim, S.H., Fantuzzi, G., Reznikov, L.L., Dinarello, C.A.

AUTHORS

and Rubinstein, M.

TITLE

Direct Submission

JOURNAL

Submitted (04-DEC-1998) Molecular Genetics, Weizmann Institute of

MEDLINE

Science, P.O. Box 26, Rehovot 76100, Israel

AUTHORS

Location/Qualifiers

FEATURES

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 ORIGIN

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AX005904

LOCUS

AX005904

DEFINITION

Sequence 5 from Patent WO909063.

ACCESSION

AX005904

VERSION

AX005904.1 GI:9228888

KEYWORDS

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SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

TITLE

Rubinstein, M. and Kim, S.H.

JOURNAL

Interleukin-18 binding proteins, their preparation and use

MEDLINE

Patent: WO 909063-A 5 25-FEB-1999;

AUTHORS

RUBINSTEIN MENACHEM (IL); KIM SOO HYUN (IL)

FEATURES

Location/Qualifiers

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BASE COUNT

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Query Match

85.0%; Score 418.2; DB 6; Length 7063;

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OY 301 tgcgaagccttggtgtctggaagcagctgacccctgctgcagacagacacacttctcctgt 360
Db 1333 TGCAAGGCTTGTGTCTGTGAGAGCTGACCCCTGCTGCACAGACCAACTTCTCTGT 1392
OY 361 gtgtcgtgtgagccctggaacagctgttcagcgtcagcgtcgtcgtgcccagctcgagct 420
Db 1393 GTGCTGTGAGACCTGTGAACAGGTGTCCAGCGTCAAGTGTCTGTGCCCCAGCTGTGGG 1452
OY 421 ggg 423
Db 1453 AGG 1455
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RESULT 9

LOCUS E58837 411 bp DNA linear PAT 31-JAN-2002
DEFINITION Interleukin 18 binding protein.
ACCESSION E58837
VERSION E58837.1 GI:18629910
KEYWORDS JP 2000210087-A/3.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 411)
AUTHORS Torikoshi, K., Tanai, M. and Kurimoto, M.
TITLE Interleukin 18 binding protein
JOURNAL Patent: JP 2000210087-A 3 02-AUG-2000;
HAYASHIBARA BIOCHEM LAB INC

COMMENT

OS Homo sapiens (human)
PN JP 2000210087-A/3
PD 02-AUG-2000
PE 28-MAY-1999 JP 1999149498

PI KAKUJI TORIKOSHI, MADOKA TANAI, MASASHI KURIMOTO PC
C12N15/09, A61K31/00, A61K38/00, A61K39/395, C07K14/47, C07K14/715, PC
C07K16/18//
PC C12P21/08, C12N15/00, A61K37/02
CC
FH key Location/Qualifiers
FT source 1. 411
FT /organism='Homo sapiens (human)'.
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source 1. 411
Location/Qualifiers
1. 411
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/db_xref='taxon:9606'

BASE COUNT 81 a 138 c 114 g 78 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 9.7e-84;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ACACCTGTCTGCAGACACACACAGCTGCTCAGTTAGAAAGCAAGAGACCCC 60
OY 61 tgcctctccagcccccaagtgctcccaagcagtaagcagtgctccagcattggaagtgaac 120
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RESULT 10

LOCUS AX005906 1360 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 7 from Patent WO9909063.
ACCESSION AX005906
VERSION AX005906.1 GI:9928889
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 1360)
AUTHORS Rubinstein, M. and Kim, S.H.
TITLE Interleukin-18 binding proteins, their preparation and use
JOURNAL RUBINSTEIN MENACHEM (IL); KIM SOO HYUN (IL)
Location/Qualifiers

FEATURES
source 1. 1360
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BASE COUNT 289 a 454 c 303 g 314 t
ORIGIN

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Best Local Similarity 97.0%; Pred. No. 2.7e-56;
Matches 296; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Db 61 TGCCCTCTCCACCCCCCACTGTTCACAGCAGTAAGCAATGTGCCAGATTGGAAGTGAAC 372
OY 121 tggcagaagtggaagtgccactgaatggaagcgtgagcttctctgtgtgtgcctgcagc 180
Db 121 TGCCAGAGGTGGAAGTGCCTGTAATGGAACGCTGAGCTTATCTGTGTGCTGCACAC 432
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QY 181 cgtctcccaactcagcatcctctactgctggcgcaatggtcttcattgagcacc 240
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QY 241 ccaggccgactgtggagggagcaccagccgggaacgtggagacaggtacgcagctg 300
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Db 493 CCAGGCCGACTGTGGAGGGAGCACCAGCGGAACTGGAGACAGCCTGGGCTGAG 552
QY 301 tgcga 305
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Db 553 GGCAA 557

RESULT 11
AF215907 1726 bp mRNA linear PRI 24-MAR-2000
LOCUS AF215907
DEFINITION Homo sapiens interleukin-18 binding protein d (IL18BP) mRNA,
complete cds.
ACCESSION AF215907
VERSION AF215907.2 GI:7327285
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1726)
Kim,S.H., Eisenstein,M., Reznikov,L., Fantuzzi,G., Novick,D.,
Rubinstein,M. and Dinarello,C.A.
Structural requirements of six naturally occurring isoforms of the
IL-18 binding protein to inhibit IL-18
Proc. Natl. Acad. Sci. U.S.A. 97 (3), 1190-1195 (2000)
MEDLINE 20122593
PUBMED 10655506
REFERENCE 2 (bases 1 to 1726)
Kim,S.H., Novick,D., Dinarello,C.A. and Rubinstein,M.
Direct Submission
Submitted (14-DEC-1999) Molecular Genetics, Weizmann Institute of
Science, POBox 26, Rehovot 76100, Israel
3 (bases 1 to 1726)
Kim,S.H., Novick,D., Dinarello,C.A. and Rubinstein,M.
Direct Submission
Submitted (24-MAR-2000) Molecular Genetics, Weizmann Institute of
Science, POBox 26, Rehovot 76100, Israel
Sequence update by submitter
On Mar 24, 2000 this sequence version replaced gi:6934281.
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COMMENT Location/Qualifiers
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ORIGIN

Query Match 59.1%; Score 290.6; DB 9; Length 1726;
Best Local Similarity 97.0%; Pred. No. 2.7e-56;
Matches 296; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Db 306 TGCCCTTCCAGCCCCCAGTGTCTCCAGACAGCTAAGCAGTGTCCAGATTGGAAGTGACC 365
QY 121 tggcagaagtggagatgccaactgaaatggaacgtatgctatcctgtggtcctgacgc 180
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Db 366 TGGCAGAGGTGGAGAGTGCACCTGAATGGAACGCTGAGCTTATCTGTGGCTTGACGC 425
QY 181 cgtctcccaactcagcatcctctactgctggcgcaatggtcttcattgagcacc 240
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Db 426 CGCTTCCCACTTCAGCATCTCTACTGGTGGCAATGTTCTTCATTGAGCACCCTC 485
QY 241 ccaggccgactgtggagggagcaccagccgggaacgtggagacaggtacgcagctg 300
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Db 486 CCAGGCCGACTGTGGAGGGAGCACCAGCGGAACTGGAGACAGCCTGGGCTGAG 545
QY 301 tgcga 305
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Db 546 GGCAA 550

RESULT 12
AF154569 626 bp mRNA linear ROD 28-MAY-2000
LOCUS AF154569
DEFINITION Rattus norvegicus interleukin 18 binding protein (il18bp) mRNA,
complete cds.
ACCESSION AF154569
VERSION AF154569.1 GI:8099343
KEYWORDS
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 626)
Im,S.H., Venkatesh,N., Barchan,D., Souroujon,M.C. and Fuchs,S.
Cloning and characterization of rat IL-18 binding protein
Unpublished
2 (bases 1 to 626)
Im,S.H., Venkatesh,N., Barchan,D., Souroujon,M.C. and Fuchs,S.
Direct Submission
Submitted (26-MAY-1999) Immunology, Weizmann Institute of Science,
Herzl, Rehovot 76100, Israel
Location/Qualifiers
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/strain="Lewis"
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11..592
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/note="IL18BP; IL18 soluble receptor and antagonist"
/codon_start=1
/product="interleukin 18 binding protein"
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ORIGIN

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Best Local Similarity 78.5%; Pred. No. 2.4e-53;
Matches 346; Conservative 0; Mismatches 92; Indels 3; Gaps 1;

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Db	170	GACCACA---CTAAGCAGTAGTACCCACATTGGATGTGATCTGGCCAGAGAAAGACTGCCA	226
Oy	142	ctgaatgtgaagcttgaagttataacctgtgtgacctgcagccgcttcccacttaagcattc	201
Db	227	CTGAATVGGAACCTCATCCCTTGCTGCACATGCGCTCACGCCGCTTCCCACACTTCAGCATC	286
Oy	202	cctctatgctgtggcaatgatgtcttcaattgagcaccccccagaagcgagactgtggaaagg	261
Db	287	CTCTACTGTGGCTGGGCAATGGCTCTTCAATTAGACACCTCCAGGCCGGCTGAGSAGGGCC	346
Oy	262	agcaccagaacgggaacgltgagacacagtagcagcagtgtgtcaagaccttgtgtctgag	321
Db	347	CACACAACCCGGGAGCAGACAGAACCCAGACACTGTGTACACAGGGCCTTGGTGTGGAG	406
Oy	322	cagctgacacctgtgacctgtgacagaccacattctctgtgtgtctgtgtgagccctyaacag	381
Db	407	GAACTGACCCCTCCCTACTAAGTACCAACTCTCTCTGCTTTGTGGATCCCGGACAG	466
Oy	382	gtgtgcacgcgtcaatgtctgtccctgcccagactgtgacctgtgagtgaggaacacctgccc	441
Db	467	GTGGGCCAGTAGTACATGTCTATTCTGGCCCCAGCTCTGGGATGATTAAGACAGCCCATTC	526
Oy	442	cccaccaccaagaagccctgccc	462
Db	527	CCTTCTCAAGAAACCCCTCTCC	547
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AF110803	AF110803	873 bp	mRNA linear ROD 03-MAR-1999
LOCUS	AF110803		
DEFINITION	Mus musculus interleukin-18 binding protein d precursor (IL18BP)		
ACCESSION	AF110803		
VERSION	AF110803.1		
KEYWORDS	GI:4324935		
SOURCE			
ORGANISM	Mus musculus.		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus. Novick,D., Kim,S.H., Fantuzzi,G., Reznikov,L.L., Dinarello,C.A. and Rudinstein,M. Interleukin-18 binding protein: a novel modulator of the Th1 cytokine response Immunity 10 (1), 127-136 (1999) 99146382		
TITLE	2 (bases 1 to 873)		
JOURNAL	NOVICK,D., Kim,S.-H., Fantuzzi,G., Reznikov,L.L., Dinarello,C.A. and Rudinstein,M. Direct Submission Submitted (04-DEC-1998) Molecular Genetics, Weizmann Institute of Science, P.O. Box 26, Rehovot 76100, Israel		
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CDS	/gene="IL18BP"		
	85..660		
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	/codon_start=1		
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Best Local Similarity	78.0%;	Pred. No. 4..4e-52;
Matches 341; Conservative	0; Mismatches 93; Indels 3; Gaps 1;	
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178	ACAACTGGCCACATGCTTTACTGTGAAGCTCAAAAGACCCATGCTCTTCTGGTCTTCACCA	237
82	ttccagcagcagcagcagctgtccagcatcttggaagtgcacctgcccagaggtggaagtcca	141
238	GTCCCAA---CTAACAGGTACCCAGACTGATGTGATTTGGCCAGAAAAGAAAGTGGCA	294
142	ctgaaatgaaagctgagctatcctctgtgtgcctgacgcgccttcccaactgaagc	201
295	CTGAATGGAACCTGACCTTGCTCTGTACTGCTGCTTCACACCCCTTCCCTCACTTCAGCATC	354
202	ctctactgctgtgggaatggtttccctcaattgaagaccctccagagccagactctggaagagg	261
335	CTCTACTGGCTGGGCAATGTTCTTCAATGAGCACTCCAGGCGCGCTGAAGAGAGGGC	414
262	agcaccagcccggaagctgtggagcagcaggtacgcagctgttgcaagacctgtgtctggag	321
415	CACACAAGTCGGGAGCAGACAGAGAACACAGACACTGCTGCACAGAGGCGCTTGCTGGTGA	474
322	cagctgacccctgtgcctctgacagcaccacattctctctgtgtgcctgtgagacctggaag	381
475	GAACAGACCCCACTACGAAGTACCAACTTCTCTTTGTTGTGTGATCTGGACAA	534
382	gtgtgcacgcgtcagctgtcctgtgcccagactctgtgctctgagcttgaaaggcaacttggcc	441
535	GTGGCCGAGTATCAATCATTTCTGGCCCAAGCTCTGGATGGGTTGAACAGACGTCCGCC	594
442	cccaccagaagaagccct	458
595	CCTTCTCAAGAAACCT	611
RESULT 14		
LOCUS	BC018332	1310 bp mRNA linear ROD 06-DEC-2001
DEFINITION	Mus musculus, interferon gamma inducing factor binding protein,	
ACCESSION	BC018332	clone MGC:25760 IMAGE:4007411, mRNA, complete cds.
VERSION	BC018332.1	GI:17390775
KEYWORDS	MGC.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.	
TITLE	1 (bases 1 to 1310)	
JOURNAL	Direct Submission	
COMMENT	Submitted (03-DEC-2001) National Institutes of Health, Mammalian	
	Gene Collection (MGC), Cancer Genomics Office, National Cancer	
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,	
	USA	
	NIH-MGC Project URL: http://mgc.nci.nih.gov	
	Contact: MGC help desk	
	Email: gcgaps-remail.nih.gov	
	Tissue Procurement: Gilbert Smith, Ph.D.	
	CDNA Library Preparation: Life Technologies, Inc.	

D5 518 GTGGCCCAATCATCTCTGGCCAGCTCTGGGATGGGTTCAAGACAGCTCCGCCC 577

Db 488

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 21:48:24 ; Search time 203.01 seconds

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Title: US-09-786-130-32

Perfect score: 492

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues 3472872

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

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1	492	100.0	492	21	AAAI1002
2	492	100.0	744	21	AAAI1007
3	492	100.0	1348	20	AAAX24749
4	492	100.0	1356	21	AAAX27384
5	418.2	85.0	7063	20	AAAX24751
6	411	83.5	411	21	AAAI1004
7	290.6	59.1	1360	20	AAAX24752
8	269	54.7	495	21	AAAI1003
9	269	54.7	847	21	AAAI1011

10	235.2	47.8	351	21	AAAI1008	Mouse IL-18 bindin
11	197.8	40.2	495	21	AAAX3451	Mouse secreted exp
12	187.6	38.1	7812	20	AAAX24753	Human interleukin-
13	152	30.9	6741	23	AAAX70037	DNA encoding novel
14	152	30.9	6741	23	AAAX70037	DNA encoding novel
15	145	29.5	1038	20	AAAX24750	Human interleukin-
16	141	28.7	234	21	AAAI1006	Human IL-18 bindin
17	73	14.8	315	20	AAAX51494	Human secreted pro
18	69.6	14.1	216	20	AAAX1394	Human secreted pro
19	57	11.6	216	21	AAAI1005	Human IL-18 bindin
20	52.2	10.6	253	21	AAAI1010	Human IL-18 bindin
21	41.2	8.4	38734	20	AAAX32020	Human METH1 relate
22	41.2	8.4	38734	22	AAAC90077	AL021529 cDNA clon
23	41	8.3	4352	22	AAAX58657	Human polynucleoti
24	41	8.3	4377	22	AAAX60453	Human polynucleoti
25	38.8	7.9	336	21	AAAI1009	Mouse IL-18 bindin
26	38.8	7.9	17612	19	AAAX23494	pseudomonas xpc, O
27	38.8	7.9	17612	21	AAAI13905	pseudomonas alcali
28	38.8	7.9	17612	22	AAAX30870	pseudomonas alcali
29	38.8	7.9	17612	24	AAAD22882	pseudomonas alcali
30	38.2	7.8	44377	18	AAAX78508	Platenolide syntha
31	38.2	7.8	44377	18	AAAX80414	Platenolide syntha
32	36.8	7.5	376	22	AAAX59188	Human Immune/haema
33	36.8	7.5	612	20	AAAX42103	Human endometrium
34	36.8	7.5	2966	22	AAAX94804	Human full-length
35	36.6	7.4	609	22	AAAI17516	Fibroblast growth
36	36.6	7.4	8933	23	AAAX82236	Drosophila melanog
37	36.4	7.4	1125	23	AAAX82236	DNA encoding novel
38	36.4	7.4	2454	23	AAAX73797	DNA encoding novel
39	36.2	7.4	1248	21	AAAX87286	S. venezuelae deso
40	36.2	7.4	12441	21	AAAX87284	S. venezuelae deso
41	36.2	7.4	13613	21	AAAX87319	S. venezuelae deso
42	36	7.3	4241	22	AAAI17545	Human nervous syst
43	36	7.3	4241	22	AAAI17546	Human nervous syst
44	35.8	7.3	999	21	AAAX46596	M. smegmatis aryla
45	35.6	7.2	11820	19	AAAI18130	Human chromosome 1

ALIGNMENTS

RESULT 1	
AAAI1002	
ID	AAAI1002 standard; DNA; 492 BP.
XX	AAAI1002;
AC	28-JUL-2000 (first entry)
XX	
DT	
DE	Human mature interleukin 18 binding protein coding sequence.
XX	
KW	Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
KW	regulator; drug; sensitivity disease; organ rejection; organ transplant;
KW	autoimmune disease; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200012555-A1.
XX	
PD	09-MAR-2000.
XX	
PF	18-NOV-1998; 98WO-JP05186.
XX	
PR	01-SEP-1998; 98JP-0247588.
XX	
PR	18-NOV-1998; 98JP-0327914.
XX	
PA	(HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX	
PT	Torigoe K, Tanial M, Kurimoto M;
XX	
DR	WPI; 2000-237850/20.
XX	
DR	P-PSDB; AAY83951.
XX	

PT Interleukin 18-binding protein with activity of regulating
 PT Physiological actions of interleukin 18, useful as regulator and drug
 PT for sensitivity diseases and organ rejection and in treating diseases
 PT due to excess immune reaction
 PS Claim 6; Page 57-59; 71pp; Japanese.
 CC The invention relates to novel interleukin 18 (IL-18)-binding proteins
 CC from humans or mice which act as regulators and drugs for sensitivity
 CC diseases and organ rejection and in treating diseases due to excess
 CC immune reaction, e.g. in slowing down rejection after organ transplant,
 CC and in treating autoimmune diseases. This sequence represents the coding
 CC sequence for the mature human interleukin 12 binding protein.
 XX
 SQ Sequence 492 BP; 97 A; 171 C; 136 G; 88 T; 0 other:

Query Match 100.0%; Score 492; DB 21; Length 492;
 Best Local Similarity 100.0%; Pred. No. 1.6e-116;
 Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acactgtctgcagaccacacacagctgcactgtcctcagttagaagacaaagagcc 60
 DB 1 acactgtctgcagaccacacacagctgcactgtcctcagttagaagacaaagagcc 60
 QY 61 tggccctccagcccccagtggttcccaagcagtaagcagtgctccagcattgtgaagc 120
 DB 61 tggccctccagcccccagtggttcccaagcagtaagcagtgctccagcattgtgaagc 120
 QY 121 tggcagaagtggaagtgccactgaatgaaacgctgaacttactctgtgtgtgcccagc 180
 DB 121 tggcagaagtggaagtgccactgaatgaaacgctgaacttactctgtgtgtgcccagc 180
 QY 181 cgcttcccacacttaacatcctcactgtgctggcgaatggttccctcattagacactc 240
 DB 181 cgcttcccacacttaacatcctcactgtgctggcgaatggttccctcattagacactc 240
 QY 241 ccaagccgactgttggaaggagagccacgcccgggaacgttggaagacacagtgacgactg 300
 DB 241 ccaagccgactgttggaaggagagccacgcccgggaacgttggaagacacagtgacgactg 300
 QY 301 tgcgaagccttgctgagcagctgacacgtgcccctgtccacagaccacttctcgt 360
 DB 301 tgcgaagccttgctgagcagctgacacgtgcccctgtccacagaccacttctcgt 360
 QY 361 gtgtctgtgacacctgaacaggtgtgtccagcgttcagtcgttccctgtggccagcttgggct 420
 DB 361 gtgtctgtgacacctgaacaggtgtgtccagcgttcagtcgttccctgtggccagcttgggct 420
 QY 421 gggtgaagggaacctgtgcccccaagaagccctgcctccagccacagcagctcca 480
 DB 421 gggtgaagggaacctgtgcccccaagaagccctgcctccagccacagcagctcca 480
 QY 481 cagcagcaggggt 492
 DB 481 cagcagcaggggt 492
 RESULT 2
 AAA11007
 ID AAA11007 standard; DNA; 744 BP.
 XX
 AC AAA11007;
 XX
 DT 28-JUL-2000 (first entry)
 XX
 DE Human Interleukin 18 binding protein complete coding sequence.
 XX
 KW Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
 KW regulator; drug; sensitivity disease; organ rejection; organ transplant;
 KW autoimmune disease; ds.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH CDS 70..654
 FT /tag= a
 FT /product= "IL-18 binding protein"
 FT sig_peptide 70..159
 FT mat_peptide 160..651
 FT /tag= b
 FT /tag= c
 WO200012555-A1.
 XX
 PD 09-MAR-2000.
 XX
 PF 18-NOV-1998; 98WO-JP05186.
 XX
 PR 01-SEP-1998; 98JP-0247588.
 PR 18-NOV-1998; 98JP-0327914.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 PI Torigoe K, Tanial M, Kurimoto M;
 XX
 DR WPI: 2000-237850/20.
 DR P-PSDB; AAY83985.
 XX
 PT Interleukin 18-binding protein with activity of regulating
 PT Physiological actions of interleukin 18, useful as regulator and drug
 PT for sensitivity diseases and organ rejection and in treating diseases
 PT due to excess immune reaction
 XX
 PS Example 2; Page 63-64; 71pp; Japanese.
 CC
 CC The invention relates to novel interleukin 18 (IL-18)-binding proteins
 CC from humans or mice which act as regulators and drugs for sensitivity
 CC diseases and organ rejection and in treating diseases due to excess
 CC immune reaction, e.g. in slowing down rejection after organ transplant,
 CC and in treating autoimmune diseases. This sequence represents the coding
 CC sequence for the full length human interleukin 12 binding protein.
 XX
 SQ Sequence 744 BP; 156 A; 249 C; 199 G; 140 T; 0 other:

Query Match 100.0%; Score 492; DB 21; Length 744;
 Best Local Similarity 100.0%; Pred. No. 1.8e-116;
 Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acactgtctgcagaccacacacagctgcactgtcctcagttagaagacaaagagcc 60
 DB 160 acactgtctgcagaccacacacagctgcactgtcctcagttagaagacaaagagcc 219
 QY 61 tggccctccagcccccagtggttcccaagcagtaagcagtgctccagcattgtgaagc 120
 DB 220 tggccctccagcccccagtggttcccaagcagtaagcagtgctccagcattgtgaagc 279
 QY 121 tggcagaagtggaagtgccactgaatgaaacgctgaacttactctgtgtgtgcccagc 180
 DB 280 tggcagaagtggaagtgccactgaatgaaacgctgaacttactctgtgtgtgcccagc 339
 QY 181 cgcttcccacacttaacatcctcactgtgctggcgaatggttccctcattagacactc 240
 DB 340 cgcttcccacacttaacatcctcactgtgctggcgaatggttccctcattagacactc 399
 QY 241 ccaagccgactgttggaaggagagccacgcccgggaacgttggaagacacagtgacgactg 300
 DB 400 ccaagccgactgttggaaggagagccacgcccgggaacgttggaagacacagtgacgactg 459
 QY 301 tgcgaagccttgctgagcagctgacacgtgcccctgtccacagcaccacttctcgt 360
 DB 460 tgcgaagccttgctgagcagctgacacgtgcccctgtccacagcaccacttctcgt 519
 QY 361 gtgtctgtgacacctgaacaggtgtgtccagcgttcagtcgttccctgtggccagcttgggct 420
 |||||||

Db 520 gtgctcgtgacccgtgaacaggtgtgtccagcgtcgtcgtgcccagctctggt 579
QY 421 gggctgaagggaacctgtgccccaccacgaagcctgtgcccctccagccacagtc 480
Db 580 gggctgaagggaacctgtgccccaccacgaagcctgtgcccctccagccacagtc 639
QY 481 cagcagcaggggt 492
Db 640 cagcagcaggggt 651

RESULT 3
AAAX24749
ID AAAX24749 standard; cDNA; 1348 BP.
XX
AC AAAX24749;
XX
DT 21-JUN-1999 (first entry)
XX
DE Human Interleukin-18 binding protein splice variant IL-18BPA cDNA.
XX
KW Interleukin-18 binding protein; IL-18BP; IL-18BPA; splice variant;
KW human; autoimmune disease; inflammation; diabetes; pancreatitis;
KW rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis;
KW psoriasis; inflammatory bowel disease; multiple sclerosis;
KW ischemic heart disease; ischemic brain injury; gene therapy; ss.
XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT CDS 66..644
FT FT /*tag= a
FT FT /product= "IL-18BPA"
FT sig_peptide 66..149
FT FT /*tag= b
FT mat_peptide 150..641
FT FT /*tag= c

PN WO909063-A1.
XX
PD 25-FEB-1999.
XX
PF 13-AUG-1998; 98WO-IL00379.
XX
PR 22-JUL-1998; 98IL-0125463.
PR 14-AUG-1997; 97IL-0121554.
PR 27-AUG-1997; 97IL-0121639.
PR 29-SEP-1997; 97IL-0121860.
PR 06-NOV-1997; 97IL-0122134.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Dlnarello C, Kim SH, Novick D, Rubinstein M;
XX
DR WPI; 1999-180975/15.
XX
P-PSDB; AAM98004.

PT New interleukin-18 binding protein - useful for treating human
PT diseases, including autoimmune disease and inflammation
XX
XX
PS Claim 12; Page 52-53; 100pp; English.
XX
XX
CC The present sequence represents a cDNA clone coding for a human
CC interleukin-18 binding protein (IL-18BP) splice variant designated
CC IL-18BPA (see AAM98004). This is one of 4 novel splice variants (see
CC AAAX24749-52), all coding for putative soluble proteins (see
CC AAM98004-07), that were detected following a screening of human
CC peripheral blood monocyte, Jurkat T-cell, peripheral blood
CC mononuclear cell and spleen cell cDNA libraries using a probe
CC produced using IL-18BP-specific primers. IL-18BPA is the most
CC abundant of the 4 splice variants and is a putative member of the
CC immunoglobulin superfamily. IL-18BP polypeptides capable of
CC binding IL-18 and/or modulating and/or blocking IL-18 activity are

CC provided. Methods for their isolation and recombinant production,
CC DNA vectors expressing them, vectors useful for their expression in
CC humans and other mammals, and antibodies against them are also
CC provided. IL-18BP polypeptides, and DNA encoding them, can be used
CC to treat conditions requiring the protein (claimed). Conditions
CC include autoimmune diseases, type I diabetes, rheumatoid arthritis,
CC graft rejections, inflammatory bowel disease, sepsis, multiple
CC sclerosis, ischemic heart diseases, ischemic brain injury, chronic
CC hepatitis, psoriasis and chronic/acute pancreatitis. IL-18BP is
CC also useful for purifying IL-18 (claimed).
XX
SQ Sequence 1348 BP; 304 A; 449 C; 292 G; 303 T; 0 other;

Query Match 100.0%; Score 492; DB 20; Length 1348;
Best Local Similarity 100.0%; Pred. No. 2.1e-116;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acacgtgtctgcagaccacacagctgtccactgtgcccctcaagttagaagacaaaggacc 60
Db 150 acacgtgtctgcagaccacacagctgtccactgtgcccctcaagttagaagacaaaggacc 209
QY 61 tgcacctccagcccccagctgttcccaagcagtaagcagtgctccagcatgtgaagtacc 120
Db 210 tgcacctccagcccccagctgttcccaagcagtaagcagtgctccagcatgtgaagtacc 269
QY 121 tggccagaggttggaagtgcacactgaatggaagctgtactatctgtgtgacctgagc 180
Db 270 tggccagaggttggaagtgcacactgaatggaagctgtactatctgtgtgacctgagc 329
QY 181 cgcttccccaacttcagacatccttactgtgtgcatgtgttccttcattgagcactc 240
Db 330 cgcttccccaacttcagacatccttactgtgtgcatgtgttccttcattgagcactc 389
QY 241 ccagggccgactgtggaggggagcaccagccgggaagctgtggagcacaggtacgacgtg 300
Db 390 ccagggccgactgtggaggggagcaccagccgggaagctgtggagcacaggtacgacgtg 449
QY 301 tgcgaagccttgtgtgtggtgagcagctgacccctgtgacagcagcaacttctcctgt 360
Db 450 tgcgaagccttgtgtgtggtgagcagctgacccctgtgacagcagcaacttctcctgt 509
QY 361 gtgctcgtgacccgtgaacaggtgtgtccagcgtcagctgtcctgtgcccagctctggt 420
Db 510 gtgctcgtgacccgtgaacaggtgtgtccagcgtcagctgtcctgtgcccagctctggt 569
QY 421 gggctgaagggaacctgtgccccaccacgaagcctgtgcccctccagccacagtc 480
Db 570 gggctgaagggaacctgtgccccaccacgaagcctgtgcccctccagccacagtc 629
QY 481 cagcagcaggggt 492
Db 630 cagcagcaggggt 641

RESULT 4
AAAX27384
ID AAAX27384 standard; cDNA; 1356 BP.
XX
AC AAAX27384;
XX
DT 16-AUG-2000 (first entry)
XX
DE Human IGFAM-4 immunoglobulin coding sequence.
XX
KW Human; immunoglobulin; IGFAM-4; IGFAM; immune disorder; cancer;
KW infection; inflammation; haematopoiesis; AIDS; allergy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 92..676
FT FT /*tag= a

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FT      sig_peptide      /product= "IGFAM-4"
FT      mat_peptide      /*tag= b
FT      242..673         /tag= c
FT      WO200029583-A2.
XX      25-MAY-2000.
XX      19-NOV-1999;      99WO-US27566.
XX      19-NOV-1998;      99US-0113635.
XX      22-DEC-1998;      98US-0113635.
XX      07-APR-1999;      99US-0128194.
XX      (INCY-) INCYTE PHARM INC.
XX      Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;
XX      Lu DM, Lal P, Hillman JL, Yang J;
XX      WPI: 2000-387796/33.
XX      P-PSDB: AAY96292.
XX      Immunoglobulin superfamily proteins, the agonist and antagonist of the
XX      protein is useful for preventing and treating disorders associated with
XX      altered levels of the protein such as cancer, immune system disorders
XX      Claim 9; Page 96; 105pp; English.
XX      The present sequence is the human immunoglobulin superfamily protein
XX      IGFAM-4 gene, which was isolated from a cDNA library of prostate tumour
XX      tissue. It is expressed in nervous, haematopoietic and immune and
XX      cardiovascular tissue, where cancer and inflammation are common. The
XX      gene, protein, its antibodies, agonists and antagonists are suitable for
XX      diagnosing and treating many diseases, including cancer, immune system
XX      disorders (such as inflammation, AIDS, allergies, anaemia,
XX      arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's
XX      disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,
XX      multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,
XX      systemic lupus erythematosus and ulcerative colitis), complications of
XX      cancer, haemodialysis and extracorporeal circulation, trauma and
XX      haematopoietic cancer (such as leukaemia) and infections caused by
XX      bacteria, viruses, fungi or parasites.
XX      Sequence 1356 BP; 282 A; 458 C; 305 G; 311 T; 0 other;

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Query Match      100.0%; Score 492; DB 21; Length 1356;
Best Local Similarity 100.0%; Pred. No. 2,1e-116;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1  acacgtgtctgcagacacacacacagctgcacgtcctcagctagtagaagacaaagacc 60
DB      182  acactgtctgcagacacacacacagctgcacgtcctcagctagtagaagacaaagacc 241
QY      61  tgcctccagcagcccccagtttcccaagacctaagcaggttccaagattggaattgacc 120
DB      242  tgcctccagcagcccccagtttcccaagacctaagcaggttccaagattggaattgacc 301
QY      121  tgcacagagtgtagagtgccacgtaatgtagcgtgaactatccctgtgtgctgcagc 180
DB      302  tgcacagagtgtagagtgccacgtaatgtagcgtgaactatccctgtgtgctgcagc 361
QY      181  cgtctcccaacttcagatcctctactgtgctggcaatggttctcattgagacacc 240
DB      362  cgtctcccaacttcagatcctctactgtgctggcaatggttctcattgagacacc 421
QY      241  ccagagccgactgtggagggagacacacagccgggaacgttggagacacaggtacgactg 300
DB      422  ccagagccgactgtggagggagacacacagccgggaacgttggagacacaggtacgactg 481

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QY      301  tcgaagccttgctgctgtagagcagctgacccctgcctgcacagacacaaattctctgt 360
DB      482  tcgaagccttgctgctgtagagcagctgacccctgcctgcacagacacaaattctctgt 541
QY      361  gtgtctgtgacccttgaacaggtgttcacaggtcactgactgtgtgcccagcttgggt 420
DB      542  gtgtctgtgacccttgaacaggtgttcacaggtcactgactgtgtgcccagcttgggt 601
QY      421  gggctgagggcaaccttgcctcccccacacaaagagccctgcctcagcagcagtcaca 480
DB      602  gggctgagggcaaccttgcctcccccacacaaagagccctgcctcagcagcagtcaca 661
QY      481  cagcagcagaggt 492
DB      662  cagcagcagaggt 673

RESULT 5
AXX24751
ID      AAX24751 standard; cDNA; 7063 BP.
XX      AAX24751;
XX      21-JUN-1999 (first entry)
XX      Human interleukin-18 binding protein splice variant IL-18Bpc cDNA.
XX      Interleukin-18 binding protein; IL-18BP; IL-18Bpc; splice variant;
XX      human; autoimmune disease; inflammation; diabetes; pancreatitis;
XX      rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis;
XX      psoriasis; inflammatory bowel disease; multiple sclerosis;
XX      ischemic heart disease; ischemic brain injury; gene therapy; ss.
XX      Homo sapiens.
XX      OS
XX      Key      Location/Qualifiers
XX      CDS      949..1542
XX      FT      /*tag= a
XX      FT      /product= "IL-18Bpc"
XX      FT      949..1032
XX      FT      /*tag= b
XX      FT      mat_peptide 1033..1539
XX      FT      /*tag= c
XX      WO9909063-A1.
XX      PN
XX      25-FEB-1999.
XX      PD
XX      PF      13-AUG-1998; 98WO-IL00379.
XX      PR      22-JUL-1998; 98IL-0125463.
XX      PR      14-AUG-1997; 97IL-0121554.
XX      PR      27-AUG-1997; 97IL-0121639.
XX      PR      29-SEP-1997; 97IL-0121860.
XX      PR      06-NOV-1997; 97IL-0122134.
XX      PA      (YEDA ) YEDA RES & DEV CO LTD.
XX      PI      Dinarello C, Kim SH, Novick D, Rubinstein M;
XX      DR      WPI: 1999-180975/15.
XX      DR      P-PSDB: AAW98006.
XX      PT      New interleukin-18 binding protein - useful for treating human
XX      PS      diseases, including autoimmune disease and inflammation
XX      Claim 12; Page 55-58; 100pp; English.
XX      The present sequence represents a cDNA clone coding for a human
XX      interleukin-18 binding protein (IL-18BP) splice variant designated
XX      IL-18Bpc (see AAW98006). This is one of 4 novel splice variants (see
XX      AAX24749-52), all coding for putative soluble proteins (see
XX      AAW98004-07), that were detected following a screening of human

```

CC peripheral blood monocyte, Jurkat T-cell, peripheral blood
 CC mononuclear cell and spleen cell cDNA libraries using a probe
 CC produced using IL-18BP-specific primers. IL-18BP is a low
 CC abundance splice variant. IL-18BP polypeptides capable of
 CC binding IL-18 and/or modulating and/or blocking IL-18 activity are
 CC provided. Methods for their isolation and recombinant production,
 CC DNA vectors expressing them, vectors useful for their expression in
 CC humans and other mammals, and antibodies against them are also
 CC provided. IL-18BP polypeptides, and DNA encoding them, can be used
 CC to treat conditions requiring the protein (claimed). Conditions
 CC include autoimmune diseases, type I diabetes, rheumatoid arthritis,
 CC graft rejections, inflammatory bowel disease, sepsis, multiple
 CC sclerosis, ischemic heart diseases, ischemic brain injury, chronic
 CC hepatitis, psoriasis, and chronic/acute pancreatitis. IL-18BP is
 CC also useful for purifying IL-18 (claimed).

XX Sequence 7063 BP; 1538 A; 2025 C; 1981 G; 1519 T; 0 other;

Query Match 85.0%; Score 418.2; DB 20; Length 7063;

Best Local Similarity 99.3%; Pred. No. 2.5e-97;

Matches 420; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 acacgtgtctgcagaccacacagctgcactgcctcagttagaagacacaaagagccc 60
 Db 1033 acacgtctctgcagaccacacagctgcactgcctcagttagaagacacaaagagccc 1092

QY 61 tggcctccagagccccaatgtttccagacagctaaagcattgtccagattggagagc 120
 Db 1093 tggcctccagagccccaatgtttccagacagctaaagcattgtccagattggagagc 1152

QY 121 tggcagaggtggaagtgcacactgaatggaacgtgagcttaccctgtgtgagcctcagc 180
 Db 1153 tggcagaggtggaagtgcacactgaatggaacgtgagcttaccctgtgtgagcctcagc 1212

QY 181 cgtctcccaacttcagacatcctctactgtgctggagcaatggttccattgagcacctc 240
 Db 1213 cgtctcccaacttcagacatcctctactgtgctggagcaatggttccattgagcacctc 1272

QY 241 ccagagccgactgtggagagggagacacacgcccggagacgtggagagacagtaagcagctg 300
 Db 1273 ccagagccgactgtggagagggagacacacgcccggagacgtggagagacagtaagcagctg 1332

QY 301 tgcgaagccttggtgtgtagcagctgacccctggccctgcacagacccaactctctctgt 360
 Db 1333 tgcgaagccttggtgtgtagcagctgacccctggccctgcacagacccaactctctctgt 1392

QY 361 gtgtctgtggaacctgaacaggtgtgtccagcgttcacgtctgtccctggccagctctggcct 420
 Db 1393 gtgtctgtggaacctgaacaggtgtgtccagcgttcacgtctgtccctggccagctctggcct 1452

QY 421 ggg 423
 Db 1453 agg 1455

RESULT 6
 ID AAA11004 standard; DNA; 411 BP.

XX AAA11004;

DT 28-JUL-2000 (first entry)

DE Human IL-18 binding protein 5' RACE fragment #1.

XX Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;

XX regulator; drug; sensitivity disease; organ rejection; organ transplant;

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..411
 FT /tag= a
 FT /partial
 FT /note="fragment of N-terminus of IL-18 binding protein"

PN WO200012555-A1.

PN 09-MAR-2000.

PF 18-NOV-1998; 98WO-JP05186.

PR 01-SEP-1998; 98JP-0247588.

PR 18-NOV-1998; 98JP-0327914.

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

PI Toriigoe K, Tanai M, Kurimoto M;

DR WPI; 2000-237850/20.

DR P-PSDB; AAY83982.

PS Example 2; Page 60-61; 71pp; Japanese.

CC The invention relates to novel interleukin 18 (IL-18)-binding proteins
 CC from humans or mice which act as regulators and drugs for sensitivity
 CC diseases and organ rejection and in treating diseases due to excess
 CC immune reaction, e.g. in slowing down rejection after organ transplant,
 CC and in treating autoimmune diseases. This sequence represents the initial
 CC fragment isolated by a 5' RACE (Rapid Amplification of cDNA Ends)
 CC reaction for the 5' end of the interleukin 12 binding protein coding
 CC sequence.

XX Sequence 411 BP; 81 A; 138 C; 114 G; 78 T; 0 other;

Query Match 83.5%; Score 411; DB 21; Length 411;

Best Local Similarity 100.0%; Pred. No. 8.1e-96;

Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acacgtgtctgcagaccacacagctgcactgcctcagttagaagacacaaagagccc 60
 Db 1 acacgtgtctgcagaccacacagctgcactgcctcagttagaagacacaaagagccc 60

QY 61 tggcctccagagccccaatgtttccagacagctaaagcattgtccagattggagagc 120
 Db 61 tggcctccagagccccaatgtttccagacagctaaagcattgtccagattggagagc 120

QY 121 tggcagaggtggaagtgcacactgaatggaacgtgagcttaccctgtgtgagcctcagc 180
 Db 121 tggcagaggtggaagtgcacactgaatggaacgtgagcttaccctgtgtgagcctcagc 180

QY 181 cgtctcccaacttcagacatcctctactgtgtggagcaatggttccattttagacaccc 240
 Db 181 cgtctcccaacttcagacatcctctactgtgtggagcaatggttccattttagacaccc 240

QY 241 ccagagccgactgtggagagggagacacacgcccggagacgtggagagacagtaagcagctg 300
 Db 241 ccagagccgactgtggagagggagacacacgcccggagacgtggagagacagtaagcagctg 300

QY 301 tgcgaagccttggtgtgtagcagctgacccctggccctgcacagacccaactctctctgt 360
 Db 301 tgcgaagccttggtgtgtagcagctgacccctggccctgcacagacccaactctctctgt 360

QY 361 gtgtctgtggaacctgaacaggtgtgtccagcgttcacgtctgtccctggccag 411
 Db 361 gtgtctgtggaacctgaacaggtgtgtccagcgttcacgtctgtccctggccag 411

RESULT 7
 AAX24752
 ID AAX24752 standard; cDNA; 1360 BP.
 XX
 AC AAX24752;
 XX
 DT 21-JUN-1999 (first entry)
 XX
 DE Human Interleukin-18 binding protein splice variant IL-18BPd cDNA.
 XX
 KW Interleukin-18 binding protein; IL-18BP; IL-18BPd; splice variant;
 KW human; autoimmune disease; inflammation; diabetes; pancreatitis;
 KW rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis;
 KW psoriasis; inflammatory bowel disease; multiple sclerosis;
 KW ischemic heart disease; ischemic brain injury; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 169..654
 FT /tag= a
 FT /product= "IL-18BPd"
 FT sig_peptide 169..252
 FT /tag= b
 FT mat_peptide 253..651
 FT /tag= c
 XX
 PN MO909063-A1.
 XX
 PD 25-FEB-1999.
 XX
 PF 13-AUG-1998; 98WO-IL00379.
 XX
 PR 22-JUL-1998; 98IL-0125463.
 PR 14-AUG-1997; 97IL-0121554.
 PR 27-AUG-1997; 97IL-0121639.
 PR 29-SEP-1997; 97IL-0121860.
 PR 06-NOV-1997; 97IL-0122134.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI DiNarello C, Kim SH, Novick D, Rubinstein M;
 XX
 DR WPI: 1999-180975/15.
 DR P-PSDB: AAW98007.
 XX
 PT New interleukin-18 binding protein - useful for treating human
 PT diseases, including autoimmune disease and inflammation
 XX
 PS Claim 12; Page 59; 100pp; English.
 XX
 CC The present sequence represents a cDNA clone coding for a human
 CC interleukin-18 binding protein (IL-18BP) splice variant designated
 CC IL-18BPd (see AAW98007). This is one of 4 novel splice variants (see
 CC AAX24749-52), all coding for putative soluble proteins (see
 CC AAW98004-07), that were detected following a screening of human
 CC peripheral blood monocyte, Jurkat T-cell, peripheral blood
 CC mononuclear cell and spleen cell cDNA libraries using a probe
 CC produced using IL-18BP-specific primers. IL-18BPd is a low
 CC abundance splice variant. IL-18BP polypeptides capable of
 CC binding IL-18 and/or modulating and/or blocking IL-18 activity are
 CC provided. Methods for their isolation and recombinant production,
 CC DNA vectors expressing them, vectors useful for their expression in
 CC humans and other mammals, and antibodies against them are also
 CC provided. IL-18BP polypeptides, and DNA encoding them, can be used
 CC to treat conditions requiring the protein (claimed). Conditions
 CC include autoimmune diseases, type I diabetes, rheumatoid arthritis,
 CC graft rejections, inflammatory bowel disease, sepsis, multiple
 CC sclerosis, ischemic heart diseases, ischemic brain injury, chronic
 CC hepatitis, psoriasis, and chronic/acute pancreatitis. IL-18BP is
 CC also useful for purifying IL-18 (claimed).
 XX
 SQ Sequence 1360 BP; 289 A; 454 C; 303 G; 314 T; 0 other;

Query Match 59.1%; Score 290.6; DB 20; Length 1360;
 Best Local Similarity 97.0%; Pred. No. 7.1e-65;
 Matches 296; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 QY 1 aacacgtctgcagagccacacagctgcactgtcctcaggttaagaagcaagaagcc 60
 DB 253 aacacgtctgcagagccacacagctgcactgtcctcaggttaagaagcaagaagcc 312
 QY 61 tgcctcccaagcccccagctgtcccaagagtaagcaagtcagcagattggaagtacc 120
 DB 313 tgcctcccaagcccccagctgtcccaagagtaagcaagtcagcagattggaagtacc 372
 QY 121 tggccagaggtggaagtgcactgaatggaacgtcgaactatccctgtgtgcccagc 180
 DB 373 tggccagaggtggaagtgcactgaatggaacgtcgaactatccctgtgtgcccagc 432
 QY 181 cgtccccaacttcagatcctctactgctggtgcaatggtctccttaattgagcctc 240
 DB 433 cgtccccaacttcagatcctctactgctggtgcaatggtctccttaattgagcctc 492
 QY 241 ccaggcgactgtgggagggagacacagccgagacgtgggagacagtaacgagctg 300
 DB 493 ccaggcgactgtgggagggagacacagccgagacgtgggagacagtaacgagctg 552
 QY 301 tgcaa 305
 DB 553 ggcac 557
 RESULT 8
 AAX11003
 ID AAX11003 standard; DNA; 495 BP.
 XX
 AC AAX11003;
 XX
 DT 28-JUL-2000 (first entry)
 XX
 DE Mouse mature Interleukin 18 binding protein coding sequence.
 XX
 KW Immunosuppressant; interleukin 18 binding protein; IL18-BP; mouse;
 KW regulator; drug; sensitivity disease; organ rejection; organ transplant;
 KW autoimmune disease; ss.
 XX
 OS Mus musculus.
 XX
 PN W0200012555-A1.
 XX
 PD 09-MAR-2000.
 XX
 PF 18-NOV-1998; 98WO-JP05186.
 XX
 PR 01-SEP-1998; 98JP-0247588.
 PR 18-NOV-1998; 98JP-0327914.
 XX
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 XX
 PI Torioge K, Tanai M, Kurimoto M;
 XX
 DR WPI: 2000-237850/20.
 XX
 PT Interleukin 18-binding protein with activity of regulating
 PT physiological actions of interleukin 18, useful as regulator and drug
 PT for sensitivity diseases and organ rejection and in treating diseases
 PT due to excess immune reaction -
 XX
 PS Claim 6; Page 57-59; 71pp; Japanese.
 XX
 CC The invention relates to novel interleukin 18 (IL-18)-binding proteins
 CC from humans or mice which act as regulators and drugs for sensitivity
 CC diseases and organ rejection and in treating diseases due to excess
 CC immune reaction, e.g. in slowing down rejection after organ transplant,

DE Mouse IL-18 binding protein 5' RACE fragment #1.
KW Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
KW regulator; drug; sensitivity disease; organ rejection; organ transplant;
KW autoimmune disease; rapid amplification of cDNA ends; RACE; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT CDS 1..351
FT /tag=a
FT /partial
FT /note="fragment of N-terminus of IL-18 binding protein"
XX
XX WO200012555-A1.
XX
XX 09-MAR-2000.
XX
XX 18-NOV-1998; 98WO-JP05186.
XX
XX 01-SEP-1998; 98JP-0247588.
XX
XX 18-NOV-1998; 98JP-0327914.
XX
XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX Toriigoe K, Tanai M, Kurimoto M;
XX
XX WPI: 2000-237850/20.
XX
XX P-PSDB: AAY83986.
XX
XX Interleukin 18-binding protein with activity of regulating
XX physiological actions of interleukin 18, useful as regulator and drug
XX for sensitivity diseases and organ rejection and in treating diseases
XX due to excess immune reaction
XX
XX Example 4; Page 65; 71pp; Japanese.
XX
XX The invention relates to novel interleukin 18 (IL-18)-binding proteins
XX from humans or mice which act as regulators and drugs for sensitivity
XX diseases and organ rejection and in treating diseases due to excess
XX immune reaction, e.g. in slowing down rejection after organ transplant,
XX and in treating autoimmune diseases. This sequence represents the initial
XX fragment isolated by a 5' RACE (Rapid Amplification of cDNA Ends)
XX reaction for the 5' end of the mouse interleukin 12 binding protein
XX coding sequence.
XX
XX Sequence 351 BP; 82 A; 103 C; 90 G; 76 T; 0 other;
SQ
Query Match 47.8%; Score 235.2; DB 21; Length 351;
Best Local Similarity 80.2%; Pred. No. 7.4e-51;
Matches 276; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 89 cagctaaagcgtgtccacatgtgaagtgacctggccagaggtggaagtcacatgaatg 148
DB 8 caactaaagcagtaaccacgactgtgattggccgaagaagaatgacacatgaatg 67
QY 149 gaacgctgactatcctgtgtgctgacagcgcttcccaacttcagcatcctact 208
DB 68 gaactctgactctgtctactgactgacagcgcttccctactcagcatcctact 127
QY 209 ggcctgggaatgtgtctctctatgtagcactcccaagcgacactgtggagggaagaca 268
DB 128 ggcctgggaatgtgtctctctatgtagcactcccaagcgacactgtggagggaagaca 187
QY 269 gccgggaacgtgtggagagcaggtacgacgtgtgcaagcgcttggtgtgagacagctga 328
DB 188 gtccgagacagaaagcaagacacgtgtgacagagcgcttgggtgaaagaaactga 247
QY 329 cccctgacctgcacagacacacacttctctgtgtgctgtgagacctaaacagttgtcc 388
DB 248 gccccacacctgagatcacacttctctgtgtgtgtgtgagaccctggaacaagtgtgcc 307

QY 389 agcgtacagctgtcctgtgccagctctgtggctgtgagtgagga 432
DB 308 agtatcacatcttgcctgtccacgctctgtgagtgagga 351
RESULT 11
ID AAA43451 standard; CDNA; 495 BP.
XX
XX AAA43451;
XX
XX 21-AUG-2000 (first entry)
XX
XX Mouse secreted expressed sequence tag SEQ ID NO:26.
XX
XX Human; mouse; chicken; rat; secreted expressed sequence tag; SEST;
XX expressed sequence tag; EST; probe; chemotactic; proliferative;
XX immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic;
XX thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal;
XX antiviral; antidiabetic; antiasthmatic; vulnerrary; antiparkinsonian;
XX antitumor; osteoprotective; neuroprotective; nootropic; antipsoriatic;
XX cerebroprotective; anticonvulsant; antidepressant; gene therapy;
XX vaccine; autoimmune disorder; multiple sclerosis; allergic condition;
XX insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
XX lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
XX central nervous system disorder; Alzheimer's disease; stroke;
XX Parkinson's disease; Huntington's disease; coagulation disorder;
XX haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
XX tumour; infection; depression; psoriasis; ss.
XX
XX Mus musculus.
XX
XX WO200021991-A1.
XX
XX 20-APR-2000.
XX
XX 15-OCT-1999; 99WO-US24206.
XX
XX 15-OCT-1998; 98US-0104436.
XX
XX (GENY) GENETICS INST INC.
XX
XX Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;
XX Metberg D, Treacy M, Bowman MR;
XX
XX WPI: 2000-317938/27.
XX
XX Isolated polynucleotides, and encoded proteins, comprising secreted
XX expressed sequence tags (ESTs), useful for treating various disorders -
XX such as autoimmune, infectious, and central nervous system disorders -
XX
XX Claim 1; Page 209; 803pp; English.
XX
XX AAA43426 to AAA45925 represent specifically claimed secreted expressed
XX sequence tags (ESTs), isolated from human, mouse, chicken and rat
XX tissue sources. The ESTs can have a range of activities depending on
XX the tissues they were isolated from. The activities include:
XX chemotactic; proliferative; immunomodulatory; haematopoietic;
XX chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory;
XX cytostatic; antibacterial; antifungal; antiviral; antidiabetic;
XX antiasthmatic; vulnerrary; antitumor; osteopathic; neuroprotective;
XX nootropic; antiparkinsonian; antipsoriatic; cerebroprotective;
XX anticonvulsant; and antidepressant. The ESTs can be used for gene
XX therapy and in vaccines. The ESTs are useful as probes for the
XX identification and isolation of full-length cDNAs and genomic DNA
XX molecules which correspond to the ESTs. Proteins encoded by the ESTs
XX are useful in assays for determining biological activity and raising
XX antibodies. They may be useful for treatment of autoimmune disorders
XX (multiple sclerosis, insulin dependent diabetes), allergic conditions
XX (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
XX osteoporosis, osteoarthritis, central nervous system disorders
XX (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
XX disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's

Query Match	Best Local Similarity	Score 152:	DB 23:	Length 6741:
Matches 158: Conservative	94.0%	Pred. No. 3.1e-29;	Mismatches 10;	Indels 0; Gaps 0;
Db 263	gaccagccggaacagctggagcagacagctgacagcagctgtgcaagcgctgtgctgagc	322		
Db 1514	GCTCCAGCCGGGAGAGCTGGGACACAGGACAGCTGTGCAAGGCGCTTGCTGGAC	1455		
Db 323	agctgacccttgcctgcagcagcagcaacattctcgttgtgtcgtggaacctgaaacag	382		
Db 1454	AGCTAGCCCGCTCCCTCGCAGCAGCAGCAACTTCTCCTGCTGTGCTCGTGAGACCTCGAAGG	1395		
Db 383	ttgtcagcgtcagctgctgctcgtgcccagcctctggctgaggg	430		
Db 1394	TGTCTCAGGCTCAGCTGCTGCTGCGCCACAGCTTGCCCTTGCTGCTGAGG	1347		

RESULT 14

AAST0676/c

AAST0676 standard; cDNA; 7103 BP.

XX	AAAT70676;
AC	
XX	
DT	13-FEB-2002 (first entry)
XX	
DE	DNA encoding novel human diagnostic protein #6480.
XX	
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX	food supplement; medical imaging; diagnostic; genetic disorder; ss.
OS	Homo sapiens.
XX	
PM	WO200175067-A2.
PN	
PD	11-OCT-2001.
XX	
PF	30-MAR-2001; 2001MO-US08631.
XX	
PR	31-MAR-2000; 2000US-0540217.
XX	
PX	23-AUG-2000; 2000US-0649167.
PA	(HYSE-) HYSEQ INC.
XX	
PI	Dmanac RT, Liu C, Tang YT;
XX	
DR	WPI, 2001-639362/73.
XX	
DR	P-PSDB; ABG06489.
PT	New isolated polynucleotide and encoded polypeptides, useful in
PT	diagnostics, forensics, gene mapping, identification of mutations
PT	responsible for genetic disorders or other traits and to assess
PT	biodiversity -
XX	
PS	Claim 1; SEQ ID No 6480; 103pp; English.
XX	
CC	The invention relates to isolated polynucleotide (I) and
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC	and gene mapping, and in recombinant production of (II). The
CC	polynucleotides are also used in diagnostics as expressed sequence tags
CC	for identifying expressed genes. (I) is useful in gene therapy techniques
CC	to restore normal activity of (II) or to treat disease states involving
CC	((II)). (II) is useful for generating antibodies against it, detecting or
CC	quantitating a polypeptide in tissue, as molecular weight markers and as
CC	a food supplement. (II) and its binding partners are useful in medical
CC	imaging of sites expressing (II). (I) and (II) are useful for treating
CC	disorders involving aberrant protein expression or biological activity.
CC	The polypeptide and polynucleotide sequences have applications in
CC	diagnostics, forensics, gene mapping, identification of mutations
CC	responsible for genetic disorders or other traits to assess biodiversity
CC	and to produce other types of data and products dependent on DNA and
CC	amino acid sequences. AAS64197-AAS94564 represent novel human
CC	diagnostic coding sequences of the invention.
CC	Note: The sequence data for this patent did not appear in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences.
XX	
SQ	Sequence 7103 BP: 1879 A; 1805 C; 2233 G; 1185 T; 1 other:
	Query Match 30.9%; Score 152; DB 23; Length 7103;
	Best Local Similarity 94.0%; Pred. NO. 3.2e-29;
	Matches 158; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
OY	263 gcaacagccgggaacgtgaggacacagtglaagcagtgtgcagaagccttgtgtcgtagc 322 Db 1876 GCTCCAGCGCGGAACGTGGAGCACACAGTACACACTGTGCAGGCGTTGTGCTGAGC 1817
OY	323 agctaacccctgctctgcacagcaccaacttctctgtgtgtctgttgaaacctgtacaagg 382 Db 1816 AGCTAAGCCCTGCTCGACACACCAACTTCCTCTGTGTGCTGTGAGCCCTGAAACAG 1757
OY	383 ttatccagcatcacgtctctgagccagacgtcttgagtcctgaagcttgaagttgaagg 430

Db 1756 TTGTCCAGCGTCACGTGCTGCGCCAGCTTGCCTCGAGAG 1709

RESULT 15

AAAX24750
ID AAX24750 standard; cDNA: 1038 BP.

AC AAX24750;

DT 21-JUN-1999 (first entry)

DE Human Interleukin-18 binding protein splice variant IL-18BPB cDNA.

XX
KW Interleukin-18 binding protein; IL-18BP; IL-18BPB; splice variant;
KW human; autoimmune disease; inflammation; diabetes; pancreatitis;
KW rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis;
KW psoriasis; inflammatory bowel disease; multiple sclerosis;
KW ischemic heart disease; ischemic brain injury; gene therapy; ss.

OS Homo sapiens.

EH Key Location/Qualifiers

FT CDS 66..407

FT /tag= a

FT /product= "IL-18BPB"

FT sig_peptide 66..149

FT /tag= b

FT mat_peptide 150..404

FT /tag= c

PN WO9909063-A1.

PD 25-FEB-1999.

PF 13-AUG-1998; 98WO-IL00379.

PR 22-JUL-1998; 98IL-0125463.

PR 14-AUG-1997; 97IL-0121554.

PR 27-AUG-1997; 97IL-0121639.

PR 29-SEP-1997; 97IL-0121860.

PR 06-NOV-1997; 97IL-0122134.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Dinarello C, Kim SH, Novick D, Rubinstein M;

DR WPI: 1999-180975/15.

DR P-PSDB; AAW98005.

PT New interleukin-18 binding protein - useful for treating human
PT diseases, including autoimmune disease and inflammation

PS Claim 12; Page 54; 100pp; English.

XX
CC The present sequence represents a cDNA clone coding for a human
CC interleukin-18 binding protein (IL-18BP) splice variant designated
CC IL-18BPB (see AAW98005). This is one of 4 novel splice variants (see
CC AAX24749-52), all coding for putative soluble proteins (see
CC AAW98004-07), that were detected following a screening of human
CC peripheral blood monocyte, Jurkat T-cell, peripheral blood
CC mononuclear cell and spleen cell cDNA libraries using a probe
CC produced using IL-18BP-specific primers. IL-18BPB is a low
CC abundance splice variant. IL-18BP polypeptides capable of
CC binding IL-18 and/or modulating and/or blocking IL-18 activity are
CC provided. Methods for their isolation and recombinant production,
CC DNA vectors expressing them, vectors useful for their expression in
CC humans and other mammals, and antibodies against them are also
CC provided. IL-18BP polypeptides, and DNA encoding them, can be used
CC to treat conditions requiring the protein (claimed). Conditions
CC include autoimmune diseases, type I diabetes, rheumatoid arthritis,
CC graft rejections, inflammatory bowel disease, sepsis, multiple
CC sclerosis, ischemic heart diseases, ischemic brain injury, chronic

CC hepatitis, psoriasis, and chronic/acute pancreatitis. IL-18BP is
CC also useful for purifying IL-18 (claimed).

SO Sequence 1038 BP; 220 A; 361 C; 211 G; 246 T; 0 other;

Query Match

29.5%; Score 145; DB 20; Length 1038;

Best Local Similarity 100.0%; Pred. No. 1,2e-27;

Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 acacctgtctgcagaccacacagctgcactgctcagttagaagacaaaggacc 60

Db 150 acacctgtctgcagaccacacagctgcactgctcagttagaagacaaaggacc 209

OY 61 tgcctccctccagcccccagtggtcccaagcagcagtgccagcattggaagtgacc 120

Db 210 tgcctccctccagcccccagtggtcccaagcagcagtgccagcattggaagtgacc 269

OY 121 tggcagaaggtggaagtgcactga 145

Db 270 tggcagaaggtggaagtgcactga 294

Search completed: August 19, 2002, 22:51:43

Job time: 3799 sec

Db 1058 TGTCCGCGAGAGAGCGCGCCGACGCGGATATCCGACACACTGTGCTGTGCCGCTGG 1117
OY 371 accctgaacaggtgtccacgctcagctcgtcgtccagctctgggtcgtgaagg 430
Db 1118 GCCTGGAAGAGCTGTGACCTCAAGCGGACCTGCGCGGTGGCTGGCGGCGCTCTGAG 1177
OY 431 caacttgcaccccaacc 448
Db 1178 GACGGGGGCCCCGTTCC 1195

RESULT 2

US-09-479-409-29
; Sequence 29, Application US/09479409
; Patent No. 6225106
; GENERAL INFORMATION:
; APPLICANT: Gerltse, Gijshert
; APPLICANT: Quax, Wilhelmus J.
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
; TITLE OF INVENTION: EXPRESSION LEVELS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/479,409
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/911,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gjalster, Debra J
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: GC361-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-846-7620
; TELEFAX: 650-845-6504
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17612 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-479-409-29

Query Match 7.9%; Score 38.8; DB 4; Length 17612;

Best Local Similarity 55.1%; Pred. No. 0.37; Mismatches 62; Indels 0; Gaps 0;

Matches 76; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
OY 311 tgggtctgagacagctgacccctgcctgcacagcaccacacttccctgtgtgctgag 370
Db 1058 TGTCCGCGAGAGAGCGCGCCGATATCCGACACACTGTGCTGTGCCGCTGG 1117
OY 371 accctgaacaggtgtccacgctcagctcgtcgtccagctctgggtcgtgaagg 430
Db 1118 GCCTGGAAGAGCTGTGACCTCAAGCGGACCTGCGCGGTGGCTGGCGGCGCTCTGAG 1177
OY 431 caacttgcaccccaacc 448
Db 1178 GACGGGGGCCCCGTTCC 1195

RESULT 3

US-09-479-453-29

; Sequence 29, Application US/09479453
; Patent No. 6313283
; GENERAL INFORMATION:
; APPLICANT: Gerltse, Gijshert
; APPLICANT: Quax, Wilhelmus J.
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
; TITLE OF INVENTION: EXPRESSION LEVELS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/479,453
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/911,853
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gjalster, Debra J
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: GC361-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-846-7620
; TELEFAX: 650-845-6504
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17612 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-479-453-29

Query Match 7.9%; Score 38.8; DB 4; Length 17612;

Best Local Similarity 55.1%; Pred. No. 0.37; Mismatches 62; Indels 0; Gaps 0;

Matches 76; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
OY 311 tgggtctgagacagctgacccctgcctgcacagcaccacacttccctgtgtgctgag 370
Db 1058 TGTCCGCGAGAGAGCGCGCCGATATCCGACACACTGTGCTGTGCCGCTGG 1117
OY 371 accctgaacaggtgtccacgctcagctcgtcgtccagctctgggtcgtgaagg 430
Db 1118 GCCTGGAAGAGCTGTGACCTCAAGCGGACCTGCGCGGTGGCTGGCGGCGCTCTGAG 1177
OY 431 caacttgcaccccaacc 448
Db 1178 GACGGGGGCCCCGTTCC 1195

RESULT 4

US-08-804-227C-7
; Sequence 7, Application US/08804227C
; Patent No. 5876991
; GENERAL INFORMATION:
; APPLICANT: Dehoff, Bradley S.
; APPLICANT: Kuhstoss, Stuart A.
; APPLICANT: Kosteck, Paul R., Jr.
; APPLICANT: Sutton, Kimberly L.
; TITLE OF INVENTION: POLYPEPTIDE SYNTHASE GENES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THOMAS G. PLANT 1501

Db 11929 CTGAAGCCGAGCGGACACCGCGCTACTTCTCGCGGGGCTGCCACGAGCTGGAG 11870
 QY 419 ctggagctgaggggaaccttgcctcccccacccaagaagccttgcctccagccacagcagtc 478
 Db 11869 CCTTACCGGGGAGCGGACGCCCGCTGCGCCACACGAGCCTCGCGCGCGCTG 11810
 QY 479 c 479
 Db 11809 c 11809

RESULT 9
 US-09-103-840A-1
 ; Sequence 1, Application US/09103840A
 ; Patent No. 6294328
 ; GENERAL INFORMATION:
 ; APPLICANT: FLEISCHMAN, Robert D.
 ; APPLICANT: WHITE, Owen R.
 ; APPLICANT: FRASER, Claire M.
 ; APPLICANT: VENTER, John C.
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 ; TITLE OF INVENTION: TUBERCULOSIS
 ; FILE REFERENCE: 24366-20007.00
 ; CURRENT APPLICATION NUMBER: US/09/103,840A
 ; CURRENT FILING DATE: 1998-06-24
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: Patentln Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 4411529
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis
 ; OTHER INFORMATION: H37Rv
 US-09-103-840A-1

Query Match 7.3%; Score 36; DB 4; Length 4411529;
 Best Local Similarity 55.6%; Pred. No. 9;
 Matches 69; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
 QY 307 gacctgtgtctgagcagctgaccctgacctgacctgacagcacaactctctctgtgtctc 366
 Db 4156424 gacattgtgcgagcagagtgccgcgcagcagcagctgacaaactccacgcgcatatc 4156483
 QY 367 gtggaccctgaagagtgctccagcgtaacgtgtctgcccagctctggagctgtgctg 426
 Db 4156484 ggcggaactgtgtgcctatcgacatgcgcggtcaagccgtgcaagctgtgagcc 4156543
 QY 427 aggg 430
 Db 4156544 cggg 4156547

RESULT 10
 US-08-911-853-34
 ; Sequence 34, Application US/08911853
 ; Patent No. 6048710
 ; GENERAL INFORMATION:
 ; APPLICANT: Gerritse, Gijbert
 ; APPLICANT: Quax, Wilhelmus J.
 ; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
 ; TITLE OF INVENTION: EXPRESSION LEVELS
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genencor International
 ; STREET: 925 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304-1013
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/911,853
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/699,092
 FILING DATE: 16-AUG-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Glaister, Debra J
 REGISTRATION NUMBER: 33,888
 REFERENCE/DOCKET NUMBER: GC361-2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-845-7620
 TELEFAX: 650-845-6504
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1176 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-911-853-34

Query Match 7.1%; Score 35; DB 3; Length 1176;
 Best Local Similarity 56.5%; Pred. No. 17;
 Matches 65; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
 QY 311 tgggtctgagcagctgacccctgacctgacagcacaactctctctgtgtctgtg 370
 Db 1058 TGTCGCCGAGAGCGGCGGCGGATCCGCGACACCTGTCGTCGCGTGG 1117
 QY 371 accctgaacagtggtccagcgtaacgtgtctgtgcccagctctgtggtgct 425
 Db 1118 GCCTGAAGAGTGTCGACTCAAGCGGAGCTGCGCCGTGGCCGCGCT 1172

RESULT 11
 US-09-479-409-34
 ; Sequence 34, Application US/09479409
 ; Patent No. 6225106
 ; GENERAL INFORMATION:
 ; APPLICANT: Gerritse, Gijbert
 ; APPLICANT: Quax, Wilhelmus J.
 ; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
 ; TITLE OF INVENTION: EXPRESSION LEVELS
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genencor International
 ; STREET: 925 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304-1013
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/479,409
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/911,853
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Glaister, Debra J
 ; REGISTRATION NUMBER: 33,888
 ; REFERENCE/DOCKET NUMBER: GC361-2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-845-7620
 ; TELEFAX: 650-845-6504
 ; INFORMATION FOR SEQ ID NO: 34:

QY	371	acccTgaacaggtttgcacagcgtaacgtctccctgcccacagctctggcctggcct	425
Db	1118	GCCTGGAGACGtGGTCGACCTCAAGGGCGACtGGCCCGTGGCCTGGCGCGCT	1172

RESULT 13

Sequence 20, Application US/083879420
Patent No. 5939289
GENERAL INFORMATION:
APPLICANT: ERTESVAG, HELGA

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STATE: VA
COUNTRY: USA
ZIP: 22042
COMPUTER READABLE

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: COMPUTER: IBM PC compatible
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: OPERATING SYSTEM: PC-DOS/MS-DOS
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: SOFTWARE: PatentIn Release #1.0, Version #1.30
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: CURRENT APPLICATION DATA:
:
: APPLICATION NUMBER: US/08/367,942C
:
: FILING DATE: 03-MAY-1995
:

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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M.
REGISTRATION NUMBER: 28,977

```

: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-205-8000
:
: TELEFAX: 703-205-8050
:
: INFORMATION FOR SEQ ID NO: 20:
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 1155 base pairs

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-387-942C-20

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Query Match	7.18	Score 34.8	DB 2	Length 1155
Best Local Similarity	48.9%	Pred. No. 1.9		
Matches 93	Conservative	0	Mismatches 97	Indels 0
				Gaps
210	gctgggcaatgctgcttcattgagcaccccccagcgacgtgaggagggagccacag	265		
672	gcagggcgggcgtgctccacgctggggcgccctctacgacatctcgtgctgacggcgcccta	733		
270	ccgggaacgtgaggacacaggtacagcgtgtgcaaggccctgtgtgtgagcagctgac	325		
732	ctacacacacacgcttgagagggcgtggagatcagagatgagggccacgacgtccaccttcacaaa	791		
330	cccttcgacctgacagacacgaactctccctcttctgctctcttgagacccttgaagaaattatcca	385		

—

732 CGCCGAGACATACGCGCACCGCCATATCGGGGATCGCGATACGCGCGCCGAGAGTACA 832
 QY 390 gcgtcacgtc 399

RESULT 14


```
; Sequence 1, Application US/08387942C
; Patent No. 5939289
; GENERAL INFORMATION:
; APPLICANT: ERTESVAG, HELGA
; APPLICANT: VALLA, SVEIN
; APPLICANT: SKJAK-BRAEK, GUDMUND
; APPLICANT: LARSEN, BJORN
; TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
; TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: P.O. BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,942C
; FILING DATE: 09-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1809-106P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12588 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORGANISM: Azotobacter vinelandii
; STRAIN: E
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 290..1951
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2227..6438
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 6702..9695
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 9973..12588
; US-08-387-942C-1

Query Match      7.1%; Score 34.8; DB 2; Length 12588;
Best Local Similarity 48.9%; Pred. No. 3.8;
Matches 93; Conservative 0; Mismatches 97; Indels 0; Gaps 0;
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OY      390 gcgtcacgtc 399
      1 1 1 1
Db      7553 GATCCTCGAC 7562
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RESULT 15
US-08-387-942C-17
; Sequence 17, Application US/08387942C
; Patent No. 5939289
; GENERAL INFORMATION:
; APPLICANT: ERTESVAG, HELGA
; APPLICANT: VALLA, SVEIN
; APPLICANT: SKJAK-BRAEK, GUDMUND
; APPLICANT: LARSEN, BJORN
; TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
; TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: P.O. BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,942C
; FILING DATE: 09-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1809-106P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1176 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-387-942C-17

Query Match      7.0%; Score 34.6; DB 2; Length 1176;
Best Local Similarity 50.9%; Pred. No. 2.2;
Matches 82; Conservative 0; Mismatches 79; Indels 0; Gaps 0;
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OY      250 ctgtgtgaggagcaccacccgggaacgttgagacacagtgtaacgactgtgcaagc 309
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      712 CTGATCGACGGCGCGCTACTAGACACAGCCCGCAAGGCGTGTCTAAGATGACC 771

OY      310 ttggtgtgagacagtcgaacctgtccctgtgacagacacaaacttctctgtgtcgtg 369
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      772 AGCGACATCAACCCGCGAAGACGCCGATATCCACAGCAAGCGCTCTCCGGGGTCCGGGTC 831

OY      370 gaccctgaacagtglttcacagcgttcacgtgtcctgtgccc 410
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      832 TACGGCGCCGACGAGCTGACAGATCTCGATTAACCAAGATCCA 872
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Search completed: August 19, 2002, 23:00:22
Job time: 4368 sec

OM of: US-09-786-130-1 to: GenEmbl:* out-format : pfs
Date: Aug 19, 2002 11:54 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

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-MODEL=framer-p2n.model -DEV=x1h  
-O=/cgn2.1/USPRO_spool/US09786130/runat_15082002.160056.6297/app_query.fasta_1.222  
-DB=GenEmbl -QEMT=fastap -SUFFIX=rge -GAPOP=12.000 -GAPEXT=4.500  
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-ALIGN=15 -MODE=LOCAL -OUTPRT=pfs -NORM=ext -HEAPSIZE=500  
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Search information block:

Query: US-09-786-130-1
Query Length: 164
Database: GenEmbl:*
Database sequences: 1797656
Database length: 187333701
Search time (sec): 1803.670000

score_list:

Sequence	Strd	Orig	ZScore	EScore	Len	Documentation
gb_pat:E58835	+	870.00	1278.01	8.0e-63	492	E58835 Interleukin 18 binding F
gb_pr:AB019504	+	870.00	1276.60	9.6e-63	583	AB019504 Homo sapiens mRNA for
gb_pat:E58840	+	870.00	1274.65	1.2e-62	744	E58840 Interleukin 18 binding F
gb_pat:AX005906	+	870.00	1269.82	2.3e-62	1348	AX005906 Sequence 1 from Paten
gb_pr:AF110799	+	870.00	1269.82	2.3e-62	1348	AF110799 Homo sapiens interleu
gb_pr:AF122906	+	870.00	1269.78	2.3e-62	1355	AF122906 Homo sapiens MCS1L-53
gb_pr:AF110801	+	821.50	1190.58	5.9e-58	3630	AF110801 Homo sapiens interleu
gb_pat:AX005904	+	821.50	1185.18	1.2e-57	7063	AX005904 Sequence 5 from Paten
gb_pat:E58837	+	727.00	1069.53	3.3e-51	411	E58837 Interleukin 18 binding F
gb_pr:AF122908	+	638.50	924.86	3.8e-43	2528	AF122908 Homo sapiens MCS1L-53
gb_pat:AX005908	+	638.50	915.71	1.2e-42	7812	AX005908 Homo sapiens MCS1L-53
gb_pr:AF110798	+	638.50	915.22	1.3e-42	8292	AF110798 Homo sapiens interleu
gb_pr:AP002490	+	638.50	889.72	3.4e-41	19186	AP002490 Homo sapiens genom
gb_pr:AP000719	+	598.50	889.34	3.5e-41	196424	AP000719 Homo sapiens genom
gb_pat:AX005906	+	598.50	869.24	4.7e-40	1736	AX005906 Sequence 7 from Paten
gb_pr:AF215907	+	523.50	767.37	2.2e-34	626	AF215907 Homo sapiens interleu
gb_pr:AF154569	+	523.00	763.93	3.5e-34	873	AF154569 Rattus norvegicus int
gb_ro:AF110803	+	523.00	763.93	3.5e-34	873	AF110803 Mus musculus interleu
gb_ro:BC018332	+	523.00	760.64	5.3e-34	1310	BC018332 Mus musculus interleu
gb_pat:E58836	+	515.00	756.79	8.6e-34	495	E58836 Interleukin 18 binding F
gb_ro:AB019505	+	515.00	755.48	1.0e-33	582	AB019505 Mus musculus mRNA for
gb_pat:E58844	+	515.00	752.43	1.5e-33	847	E58844 Interleukin 18 binding F
gb_ro:AF122907	+	515.00	748.23	2.6e-33	1422	AF122907 Mus musculus MCS1L-53
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gb_pat:E58841	+	441.00	650.95	6.8e-28	351	E58841 Interleukin 18 binding F
gb_htg:AC098723	+	380.00	508.82	5.6e-20	228133	AC098723 Mus musculus chrom
gb_pat:AX005902	+	312.50	453.50	6.8e-17	1038	AX005902 Sequence 3 from Paten
gb_pr:AF110800	+	312.50	453.50	6.8e-17	1038	AF110800 Homo sapiens interl
gb_htg:AC097860	+	285.50	377.81	1.1e-12	88166	AC097860 Rattus norvegicus cl
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gb_v1:MC0271163	+	217.00	317.01	2.7e-09	637	AJ271163 Molluscum contagiosu
gb_v1:MC060315	+	205.00	253.38	9.5e-06	120289	U60315 Molluscum contagiosu
gb_v1:AF335258S1	-	124.00	156.56	2.34	12518	AF335258 Lumby skin disease v
gb_v1:AF335258	-	124.00	136.36	31.21	150773	AF335258 Lumby skin disease v
gb_pr:HS1158812	-	119.00	130.68	64.67	122884	AL034396 Human DNA sequence
gb_v1:XD12933568	-	115.50	124.22	148.04	144575	AI2933568 Yaba-like disease v
gb_pr:AC002293	-	109.50	131.89	55.40	19000	AC002293 Genomic sequence frc
gb_pr:AC002102	-	109.50	135.06	133.03	44078	AC002102 Homo sapiens chromo
gb_htg:AC010535	-	108.50	112.11	699.75	181233	AC010535 Homo sapiens chrom
gb_pr:AL137790	+	107.50	113.50	585.32	127409	AL137790 Human DNA sequence

gb_pr:AL445931 - 107.50 110.93 814.66 175033 i AL445931 Human DNA sequen
gb_v1:AF380138 - 107.50 109.97 920.67 196858 i AF380138 Monkeypox virus
gb_htg:AC019225 - 107.50 109.82 939.03 200627 i AC019225 Homo sapiens chr
gb_pat:AR145593 + 106.00 157.99 1.95 405 i AR145593 Sequence 45 from p
gb_pat:IS8307 + 106.00 157.99 1.95 405 i IS8307 Sequence 45 from pat

seq_name: gb_pat:E58835

seq_documentation block:

LOCUS E58835 492 bp DNA linear PAT 31-JAN-2002
DEFINITION Interleukin 18 binding protein.
ACCESSION E58835
VERSION E58835.1 GI:18629908
KEYWORDS JP 2000210087-A/1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 492)
Torikoshi, K., Tanai, M. and Kurimoto, M.
Interleukin 18 binding protein
Patent: JP 2000210087-A 1 02-AUG-2000;
HAYASHIBARA BIOCHEM LAB INC
OS Homo sapiens (human)
PN JP 2000210087-A/1
PD 02-AUG-2000
PF 28-MAY-1999 JP 1999149498

COMMENT

PR KAKUJI TORIKOSHI, MADOKA TANAI, MASASHI KURIMOTO PC
P12N15/09, A6IK31/00, A6IK38/00, A6IK39/395, C07K14/47, C07K14/715, PC
C07K16/18//
PC C12P21/08, C12N15/00, A6IK37/02

FEATURES
FT Key Location/Qualifiers
1..492 Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 97 a 171 c 136 g 88 t
ORIGIN

alignment_scores:

Quality: 870.00 Length: 164
Ratio: 5.305 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-786-130-1 x E58835 ..

Align seg 1/1 to: E58835 from: 1 to: 492

1 ThrProValSerGlnThrThrAlaAlaThrAlaSerValArgSerTh 17
|||||
1 ACACCTGCTCTGCAGACACACAGCTCCACTGCTGCTAGAGAGAC 50
|||||
17 TlyAspProCysProSerGlnProProValPheProAlaAlaLysGlnC 34
|||||
51 AAAGGACCCCGCCGCCGCCAGCCGCCAGTGTCCAGACACCTAAGCAGT 100
|||||
34 yspProAlaLeuGluValThrThrProGluValGluValProLeuAsnGly 50
|||||
101 GTCCAGCATTTGGAAGTGCCTGCGCAGAGGTGGAAGTCCACTGAATGGA 150
|||||
51 ThrLeuSerLeuSerCysValAlaCysSerArgPheProAsnPheSer1 67
|||||
151 ACAGCTAGAGCTATCTGCTGCTGCAGCGCTTCCACCTTCCAGCAT 200
|||||
67 eleuTyTrpLeuGlnGlyAsnGlySerPheTleGluHisLeuProGlyArgL 84
|||||
201 CCTCTACAGCTGGCGCAATGGTCTCTTCATTCAGACACCTCCAGCGCCAGC 250

84 eutrpuglserThrSerArgGluArgGlySerThrGlyThrGlnLeu 100
|||||
251 TGTGGAGGGGAGACACCGGGAGACGTGGGAGACAGGTACGACAGCTG 300
101 CysLysAlaLeuValLeuGlnLeuThrProAlaLeuHisSerThrAs 117
|||||
301 TGCAGAGCCTGTGCTGCTGGAGCAGCTGACCCCTGCTGGACAGCACC 350
351 CTCTCTCTGTGCTGCTGGAGCAGCTGACCCCTGCTGGACAGCACC 400
117 nphSerCysValLeuValAspProGlnValValGlnArgHisValY 134
|||||
134 alleuAlaGlnLeuTrpAlaGlyLeuArgAlaThrLeuProProThrGln 150
|||||
401 TCCTGCCCCAGCTCTGGGTGGGTGAGGCAACCTTGCCCCCACCACCA 450
151 GluAlaLeuProSerSerHisSerSerProGlnGlnGly 164
|||||
451 GAAGCCCTGCGCTCCAGCCACAGACTCCACAGCAGAGGT 492

seq_name: gb_pr:AB019504

seq_documentation_block:

LOCUS AB019504 585 bp mRNA linear PRI 31-MAR-1999
DEFINITION Homo sapiens mRNA for interleukin-18 binding protein, complete cds.
ACCESSION AB019504
VERSION AB019504.1 GI:4586394
KEYWORDS interleukin-18 binding protein.
SOURCE Homo sapiens (isolate:white) male liver cDNA to mRNA.
ORGANISM Homo sapiens

REFERENCE 1 (sites)
AUTHORS Alizawa,Y., Akita,K., Tanial,M., Korigoe,K., Mori,T., Nishida,Y.,
Ushio,S., Nukada,Y., Tanimoto,T., Ikegami,H., Ikeda,M. and
Kurimoto,M.

TITLE Cloning and expression of interleukin-18 binding protein
JOURNLM FEBS Lett. 445 (2-3), 338-342 (1999)
MEDLINE 99192308

REFERENCE 2 (bases 1 to 585)

AUTHORS Alizawa,Y.
TITLE Direct Submission
JOURNML Submitted (04-NOV-1998) Yasushi Alizawa, Hayashibara Biochemical
Laboratories, Inc., Fujisaki Institute, 675-1, Fujisaki, Okayama,
Okayama 702-8005, Japan (E-mail:fujisaki@hayashibara.co.jp,
Tel:81-86-276-3141, Fax:81-86-276-6885)
COMMENT Sequence updated (30-Nov-1998).

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CDS
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BASE COUNT 116 a 203 c 157 g 109 t
ORIGIN

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Percent Similarity: 100.000 Percent Identity: 100.000

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LOCUS E58840 744 bp DNA linear PAT 31-JAN-2002
DEFINITION Interleukin 18 binding protein.
ACCESSION E58840
VERSION E58840.1 GI:18629913
KEYWORDS JP 2000210087-A/6.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 744)
AUTHORS Torikoshi,K., Tanial,M. and Kurimoto,M.
TITLE Interleukin 18 binding protein
JOURNML Patent: JP 2000210087-A 6 02-AUG-2000;
HAYASHIBARA BIOCHEM LAB INC
COMMENT OS Homo sapiens (human)
PN JP 2000210087-A/6
PD 02-AUG-2000
PF 28-MAY-1999 JP 1999149498
PR
PI KAKUI TORIKOSHI,MADOKA TANIAI,MASASHI KURIMOTO PC
C12N15/09,A61K31/00,A61K38/00,A61K39/395,C07K14/47,C07K14/715, PC
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LOCUS AX005900 1348 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 1 from Patent WO9909063.
ACCESSION AX005900
VERSION AX005900.1 GI:9928886
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 1348)
AUTHORS Rubinstejn,M. and Kim,S.H.
TITLE Interleukin-18 binding proteins, their preparation and use
JOURNAL Patent: WO 9909063-A 1 25-FEB-1999.
RUBINSTEIN MENACHEM (IL); KIM SOO HYUN (IL)
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LOCUS AF110799 1348 bp mRNA linear PRI 03-MAR-1999
DEFINITION Homo sapiens interleukin-18 binding protein a precursor (IL18BP)
ACCESSION AF110799
VERSION AF110799.1 GI:4324927
KEYWORDS mRNA, complete cds.
SOURCE human.

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1348)
AUTHORS Novick,D., Kim,S.H., Fantuzzi,G., Reznikov,L.L., Dinarello,C.A. and
Rubinstein,M.
TITLE Interleukin-18 binding protein: a novel modulator of the Th1
cytokine response
JOURNAL Immunology 10 (1), 127-136 (1999)
MEDLINE 99146382
REFERENCE 2 (bases 1 to 1348)
AUTHORS Novick,D., Kim,S.H., Fantuzzi,G., Reznikov,L.L., Dinarello,C.A.
and Rubinstein,M.
TITLE Direct Submission
JOURNAL Submitted (04-DEC-1998) Molecular Genetics, Weizmann Institute of
Science, P.O. Box 26, Rehovot 76100, Israel
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DEFINITION Homo sapiens MC51L-53L-54L homolog mRNA, complete cds.
ACCESSION AF122906
VERSION AF122906.1 GI:5231015
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1355)
AUTHORS Xiang,Y. and Moss,B.
TITLE Identification of human and mouse homologs of the MC51L-53L-54L
family of secreted glycoproteins encoded by the Molluscum
contagiosum poxvirus
JOURNAL Virology 257 (2), 297-302 (1999)
MEDLINE 99263157
PUBMED 10329540
REFERENCE 2 (bases 1 to 1355)
AUTHORS Xiang,Y. and Moss,B.
TITLE Direct Submission
JOURNAL Submitted (25-JAN-1999) NIAID/LVD, NIH, 9000 Rockville Pike,
Bethesda, MD 20892, USA
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LOCUS AF110801 3630 bp mRNA linear PRI 03-MAR-1999
 DEFINITION Homo sapiens interleukin-18 binding protein c precursor (IL18BP)
 mRNA, complete cds.

ACCESSION AF110801 GI:4324931

VERSION

KEYWORDS

SOURCE

ORGANISM

human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

AUTHORS

Novick,D., Kim,S.-H., Fantuzzi,G., Reznikov,L.L., Dinarello,C.A. and

Rubinstein,M.

Interleukin-18 binding protein: a novel modulator of the Th1

TITLE

cytokine response

Immunity 10 (1), 127-136 (1999)

JOURNAL

MEDLINE

REFERENCE

AUTHORS

TITLE

JOURNAL

2 (bases 1 to 3630)
 Novick,D., Kim,S.-H., Fantuzzi,G., Reznikov,L.L., Dinarello,C.A.
 and Rubinstein,M.
 Direct Submission
 Submitted (04-DEC-1998) Molecular Genetics, Weizmann Institute of
 Science, P.O. Box 26, Rehovot 76100, Israel

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DEFINITION Sequence 5 from Patent WO9909063.
ACCESSION AX005904
VERSION AX005904.1 GI:9928888

KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 7063)
AUTHORS Rubinstein,M. and Kim,S.H.

TITLE Interleukin-18 binding proteins, their preparation and use
JOURNAL Patent: WO 9909063-A 5 25-FEB-1999;

RUBINSTEIN MENACHEM (IL); KIM SOO HYUN (IL)
FEATURES
Location/Qualifiers

1..7063

/organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT 1538 a 2025 c 1981 g 1519 t
ORIGIN

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Quality: 821.50 Length: 241
Ratio: 5.009 Gaps: 1
Percent Similarity: 68.050 Percent Identity: 68.050

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Align seg 1/1 to: AX005904 from: 1 to: 7063

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139 ..... 139
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seq_documentation_block:

LOCUS E58837 411 bp DNA linear PAT 31-JAN-2002
DEFINITION Interleukin 18 binding protein.
ACCESSION E58837
VERSION E58837.1 GI:18629910

KEYWORDS JP 2000210087-A/3.
SOURCE Homo sapiens.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 411)
AUTHORS Torikoshi,K., Tanai,M. and Kurimoto,M.
TITLE Interleukin 18 binding protein
JOURNAL Patent: JP 2000210087-A 3 02-AUG-2000;

HAYASHIBARA BIOCHEM LAB INC
OS Homo sapiens (human)
PN JP 2000210087-A/3

PD 02-AUG-2000
PF 28-MAY-1999 JP 1999149498

PR KAKUJI TORIKOSHI,MADOKA TANAI,MASASHI KURIMOTO PC
C12N15/09,A61K31/00,A61K38/00,A61K39/395,C07K14/47,C07K14/715, PC
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PC C12P21/08,C12N15/00,A61K37/02


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CC      Key      Location/Qualifiers
FH      source      1. .411
FT      Location/Qualifiers
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                /db_xref="taxon:9606"
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51  ThreuserLeuSerCysValAlaCysSerArgPheProAsnPheSerTII 67
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    |||||||
201  CCTTACTGGCTGGCAATGGTTCTTCATTGACACCTCCACAGCGCGAC 250
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seq_documentation_block:
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DEFINITION Homo sapiens MC51L-53L-54L homolog gene, partial cds.
ACCESSION      AF122908
VERSION      AF122908.1      GI:5231019
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1      (bases 1 to 2528)
AUTHORS      Xiang,Y. and Moss,B.
TITLE      Identification of human and mouse homologs of the MC51L-53L-54L

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JOURNAL      family of secreted glycoproteins encoded by the Mollusum
MEDLINE      Contagiosum poxvirus
PUBMED      virology 257 (2), 297-302 (1999)
REFERENCE      2      (bases 1 to 2528)
AUTHORS      Xiang,Y. and Moss,B.
TITLE      Direct Submission
JOURNAL      Submitted (25-JAN-1999) NIAID/LVD, NIH, 9000 Rockville Pike,
                Bethesda, MD 20892, USA
FEATURES
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BASE COUNT      525 a      794 c      652 g      557 t
ORIGIN

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    Ratio: 3.893      Gaps: 5
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1581 TGCTGCTTCACTTCCCTAGGCTGGGCTGAGGCAACTTGGCCCCAC 1630
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LOCUS AX005908 7812 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 9 from Patent WO9909063.
ACCESSION AX005908
VERSION AX005908.1 GI:9928890
KEYWORDS
SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
1 (bases 1 to 7812)
AUTHORS Rubinstein,M. and Kim,S.H.
JOURNAL Interleukin-18 binding proteins, their preparation and use
Patent: WO 9909063-A 9 25-FEB-1999;
RUBINSTEIN MENACHEM (IL); KIM SOO HYUN (IL)
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BASE COUNT 1689 a 2278 c 2167 g 1678 t
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Quality: 638.50 Length: 483
Ratio: 3.893 Gaps: 5
Percent Similarity: 33.954 Percent Identity: 33.540

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alignment_block:

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seq_documentation block:
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DEFINITION Homo sapiens Interleukin-18 binding protein precursor (IL18BP)
ACCESSION AF110798
VERSION AF110798.1 GI:4324923
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 8292)
AUTHORS Novick,D., Kim,S.H., Fantuzzi,G., Reznikov,L.L., Dinaarello,C.A. and
Rubinstein,M.
TITLE Interleukin-18 binding protein: a novel modulator of the Th1
JOURNAL cytokine response
MEDLINE Immunity 10 (1), 127-136 (1999)
99146382
REFERENCE 2 (bases 1 to 8292)
AUTHORS Novick,D., Kim,S.H., Fantuzzi,G., Reznikov,L.L., Dinaarello,C.A.
and Rubinstein,M.
TITLE Direct Submission
JOURNAL Submitted (04-DEC-1998) Molecular Genetics, Weizmann Institute of
Science, P.O. Box 26, Rehovot 76100, Israel
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alignment_scores:	Quality: 638.50	Length: 483			
	Ratio: 3.893	Gaps: 5			
Percent Similarity:	33.954	Percent identity:	33.540		
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US-09-786-130-1 x AF110798 ..					
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86	ugly.....	87
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sequence.
ACCESSION AP002490
VERSION AP002490.4 GI:15637090
KEYWORDS HTG.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1 (bases 1 to 191986)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens genomic DNA
2 (bases 1 to 191986)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (09-JUN-2000) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT On Sep 17, 2001 this sequence version replaced gi:15617455.
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DEFINITION Homo sapiens genomic DNA, chromosome 11q clone:RP11-757C15,
complete sequences.
ACCESSION  AP000719
VERSION    AP000719.4  GI:13094220
KEYWORDS   HTG.
SOURCE      Homo sapiens DNA, clone:RP11-757C15.
ORGANISM    Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (sites)
AUTHORS     Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
            Homo sapiens genomic DNA
            Published Only in DataBase (1999) In press
            2 (bases 1 to 196424)
TITLE       Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
            Direct Submission
            Submitted (11-NOV-1999) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
            1-7-22 Suehiro-chou,Tsukumi-Ku, Yokohama, Kanagawa 230-0045, Japan
            Tel:81-45-503-9111, Fax:81-45-503-9170)
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ACCESSION AX005906
VERSION AX005906.1 GI:9928889
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 1360)
REFERENCE
AUTHORS Rubinstein, M. and Kim, S.H.
TITLE Interleukin-18 binding proteins, their preparation and use
JOURNAL Patent: WO 9909063-A 7 25-FEB-1999;
RUBINSTEIN MENACHEM (IL); KIM SOO HYUN (IL)

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About: Results were produced by the Gencore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

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AC AA11002;

DT 28-JUL-2000 (first entry)

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KW Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;

KW regulator; drug; sensitivity disease; organ rejection; organ transplant;

KW autoimmune disease; ss.

OS Homo sapiens.

PN WO200012555-A1.

PD 09-MAR-2000.

PE 18-NOV-1998; 98WO-JP05186.

XX 01-SEP-1998; 98JP-0247588.

PR 18-NOV-1998; 98JP-0327914.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

PA Toriigoe K, Tanai M, Kurimoto M;

WP1; 2000-237850/20.

P-PSDB; AAY83951.

PT Interleukin 18-binding protein with activity of regulating

PT physiological actions of interleukin 18, useful as regulator and drug

PT for sensitivity diseases and organ rejection and in treating diseases

CC due to excess immune reaction -

PS Claim 6; Page 57-59; 71pp: Japanese.

CC The invention relates to novel interleukin 18 (IL-18)-binding proteins

CC from humans or mice which act as regulators and drugs for sensitivity

CC diseases and organ rejection and in treating diseases due to excess

CC immune reaction, e.g. in slowing down rejection after organ transplant,

CC and in treating autoimmune diseases. This sequence represents the coding

CC sequence for the mature human interleukin 12 binding protein.

SQ Sequence 492 BP; 97 A; 171 C; 136 G; 88 T; 0 other;

alignment_scores: 870.00 Length: 164

Ratio: 5.305 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block: US-09-786-130-1 x AA11002 ..

Align seg 1/1 to: AA11002 from: 1 to: 492

1 ThrProValSerGlnThrThrAlaAlaThrAlaSerValArgSerTh 17
|||||
1 ACACCTGCTCTGCAGACACACACAGCTGCCCTGCTAGTAAAGAC 50
|||||
17 TlysaspProCysProSerGlnProProValPheProAlaAlaLysGlnC 34
|||||
51 AAAGGACCCCTGCCCCCTCCAGCCCCAGTGTTCACAGCAGCTAAGCAGT 100
|||||

```

34 ysfProAlaLeuGIuVal1ThrTTPProGluVal1GluVal1ProLeuasnGly 50
   |||||||
101 GTCCACCAATTGGAAAGTACCTGGCCAGAGGTGGAAGTGCACATGAATGGA 150
51 ThrluSerleuSerCysVal1AlaCysSerArgPheProasnPheSer11 67
   |||||||
151 ACCTGAGCTTATCTGTGTGGCTGACAGCCGCTCCCAACTTCAGCAT 200
67 eLeuTyrTrpLeuGIyAsnGIySerPheIleGIuHisIleuProGIyArgL 84
   |||||||
201 CCTCTACTGGCTGGCAATGGTCTTCATTATGACACCTCCAGGGCGGAC 250
84 eutPrluGIySerThrSerArgGluArgGIySerThrGIyThrGlnLeu 100
   |||||||
251 TGTGGAGGGGAGACACACAGCCGGGAACGTGGGAGCACAGGTACGACGCTC 300
101 CysLysAlaLeuVal1LeuGIuGlnLeuThrProAlaLeuHisSerThrAs 117
   |||||||
301 TGCAGAGCCTTGCTGGTGGAGCAGCTGACCCCTGCTGCACACCA 350
117 nPheSerCysVal1LeuVal1AspProGIuGlnVal1GlnArgHisValY 134
   |||||||
351 CTCTCTCTGTGTGCTGGACCTGACACAGGTGTCCAGCGTCACGCTCG 400
134 allLeuAlaGlnLeuThrPrlaGlyLeuArgAlaThrleuProPrlGln 150
   |||||||
401 TCTTGCCCGAGCTGTGGCTGGGCTGAGGGCAACTTGGCCCCCACCACCA 450
151 GluAlaLeuProSerSerHisSerSerProGlnGlnGlnGly 164
   |||||||
451 GAAGCCCTGCTCCAGCCACAGCAGTCCACAGCAGCAGAGGT 492

seq_name: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT:AAA11007
seq_documentation_block:
ID AAA11007 standard; DNA; 744 BP.
XX
XX AAA11007;
XX
XX 28-JUL-2000 (first entry)
XX
XX Human interleukin 18 binding protein complete coding sequence.
XX
XX Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
XX Regulator; drug; sensitivity disease; organ rejection; organ transplant;
XX autoimmune disease; ds.
XX
XX Homo sapiens.
XX
XX OS
XX FH Location/Qualifiers
XX CDS 70..654
XX FT /*tag= a
XX FT /product= "IL-18 binding protein"
XX FT 70..159
XX FT /*tag= b
XX FT mat_peptide 160..651
XX FT /*tag= c
XX
XX WO200012555-A1.
XX
XX PD 09-MAR-2000.
XX
XX PF 18-NOV-1998; 98WO-JP05186.
XX
XX PR 01-SEP-1998; 98JP-0247588.
XX PR 18-NOV-1998; 98JP-0327914.
XX
XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX ToriGo K, Taniai M, Kurimoto M;
XX
XX WPI; 2000-237850/20.

```

```

DR P-PSDB; AAY83985.
XX
XX Interleukin 18-binding protein with activity of regulating
PT physiological actions of interleukin 18, useful as regulator and drug
PT for sensitivity diseases and organ rejection and in treating diseases
PT due to excess immune reaction
XX
XX Example 2; Page 63-64; 71pp; Japanese.
XX
XX The invention relates to novel interleukin 18 (IL-18)-binding proteins
CC from humans or mice which act as regulators and drugs for sensitivity
CC diseases and organ rejection and in treating diseases due to excess
CC immune reaction, e.g. in slowing down rejection after organ transplant,
CC and in treating autoimmune diseases. This sequence represents the coding
CC sequence for the full length human interleukin 12 binding protein.
XX
XX Sequence 744 BP; 156 A; 249 C; 199 G; 140 T; 0 other:

alignment_scores:
Quality: 870.00 Length: 164
Ratio: 5.305 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-786-130-1 x AAA11007 ..
Align seg 1/1 to: AAA11007 from: 1 to: 744

1 ThrlProValSerGIuThrThrAlaAlaThrAlaSerValArgSerTh 17
   |||||||
160 ACACGTGTCTCGACAGCACACACAGCTGCCACGTCTGATGAAGAC 209
17 rLysAspProCysProSerGIuProProValPheProAlaAlaLysGlnC 34
   |||||||
210 AAGAGACCCCTGGCCCTCCAGGCCAGTGTTCACAGCAGCAACAGT 259
34 ysfProAlaLeuGIuVal1ThrTTPProGluVal1GluVal1ProLeuasnGly 50
   |||||||
260 GTCCACCAATTGGAAAGTACCTGGCCAGAGGTGGAAGTGCACATGAATGGA 309
51 ThrluSerleuSerCysVal1AlaCysSerArgPheProasnPheSer11 67
   |||||||
310 ACCTGAGCTTATCTGTGTGGCTGACAGCCGCTCCCAACTTCAGCAT 359
67 eLeuTyrTrpLeuGIyAsnGIySerPheIleGIuHisIleuProGIyArgL 84
   |||||||
360 CCTCTACTGGCTGGCAATGGTCTTCATTATGACACCTCCAGGGCGGAC 409
84 eutPrluGIySerThrSerArgGluArgGIySerThrGIyThrGlnLeu 100
   |||||||
410 TGTGGAGGGGAGACACACCGGGAACGTGGGAGCACAGGTACGACGCTG 459
410 TGTGGAGGGGAGACACACCGGGAACGTGGGAGCACAGGTACGACGCTG 459
101 CysLysAlaLeuVal1LeuGIuGlnLeuThrProAlaLeuHisSerThrAs 117
   |||||||
460 TGCAGAGCCTTGCTGGTGGAGCAGCTGACCCCTGCTGCACACCA 509
560 TCTTGCCCGAGCTGTGGCTGGGCTGAGGGCAACTTGGCCCCCACCACCA 609
117 nPheSerCysVal1LeuVal1AspProGIuGlnVal1GlnArgHisValY 134
   |||||||
510 CTCTCTCTGTGTGCTGGACCTGACACAGGTGTCCAGCGTCACGCTCG 559
134 allLeuAlaGlnLeuThrPrlaGlyLeuArgAlaThrleuProPrlGln 150
   |||||||
560 TCTTGCCCGAGCTGTGGCTGGGCTGAGGGCAACTTGGCCCCCACCACCA 609
151 GluAlaLeuProSerSerHisSerSerProGlnGlnGlnGly 164
   |||||||
610 GAAGCCCTGCTCCAGCCACAGCAGTCCACAGCAGCAGAGGT 651

seq_name: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1999.DAT:AAx24749
seq_documentation_block:
ID AAx24749 standard; CDNA; 1348 BP.

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XX	AA24749;	
XX	21-JUN-1999 (first entry)	
XX	Human interleukin-18 binding protein splice variant IL-18BPA cDNA.	
DE		
XX		
XX	Interleukin-18 binding protein; IL-18BP; IL-18BPA; splice variant;	
KW	human; autoimmune disease; inflammation; diabetes; pancreatitis;	
KW	rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis;	
KW	psoriasis; inflammatory bowel disease; multiple sclerosis;	
XX	ischemic heart disease; ischemic brain injury; gene therapy; ss.	
OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	CDS	66..644
FT		/*tag= a
FT		/product= "IL-18BPA"
FT	sig_peptide	66..149
FT		/*tag= b
FT	mat_peptide	150..641
FT		/*tag= c
XX		
XX	W09909063-A1.	
PN		
XX	25-FEB-1999.	
PD		
XX	13-AUG-1998; 98MO-IL00379.	
PF		
XX	22-JUL-1998; 98IL-0125463.	
PR	14-AUG-1997; 97IL-0121554.	
PR	27-AUG-1997; 97IL-0121639.	
PR	29-SEP-1997; 97IL-0121860.	
XX	06-NOV-1997; 97IL-0122134.	
XX		
XX	(YEDA) YEDA RES & DEV CO LTD.	
PA		
PI	Dinareello C, Kim SH, Novick D, Rubinstein M;	
XX	WPI: 1999-180975/15.	
DR	P-PSDB; AAW98004.	
XX		
PT	New interleukin-18 binding protein - useful for treating human	
PT	diseases, including autoimmune disease and inflammation	
XX		
PS	Claim 12; Page 52-53; 100pp; English.	
XX		
CC	The present sequence represents a cDNA clone coding for a human	
CC	interleukin-18 binding protein (IL-18BP) splice variant designated	
CC	IL-18BPA (see AAW98004). This is one of 4 novel splice variants (see	
CC	AA24749-52), all coding for putative soluble proteins (see	
CC	AAW98004-07), that were detected following a screening of human	
CC	peripheral blood monocyte, Jurkat T-cell, peripheral blood	
CC	mononuclear cell and spleen cell cDNA libraries using a probe	
CC	produced using IL-18BP-specific primers. IL-18BPA is the most	
CC	abundant of the 4 splice variants and is a putative member of the	
CC	immunoglobulin superfamily. IL-18BP polypeptides capable of	
CC	binding IL-18 and/or modulating and/or blocking IL-18 activity are	
CC	provided. Methods for their isolation and recombinant production, in	
CC	DNA vectors expressing them, vectors useful for their expression in	
CC	humans and other mammals, and antibodies against them are also	
CC	provided. IL-18BP polypeptides, and DNA encoding them, can be used	
CC	to treat conditions requiring the protein (claimed). Conditions	
CC	include autoimmune diseases, type I diabetes, rheumatoid arthritis,	
CC	graft rejections, inflammatory bowel disease, sepsis, multiple	
CC	sclerosis, ischemic heart diseases, ischemic brain injury, chronic	
CC	hepatitis, psoriasis, and chronic/acute pancreatitis. IL-18BP is	
CC	also useful for purifying IL-18 (claimed).	
XX		
Sequence 1348 BP; 304 A; 449 C; 292 G; 303 T; 0 other;		

alignment_scores:			
Quality:	870.00	Length:	154
Ratio:	5..305	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000
alignment_block:			
US-09-786-130-1 x AAX24749	..		
Align seg 1/1 to: AAX24749	from: 1 to: 1348		
1 ThrProValSerGlnThrThrThrAlaAlaThrAlaSerValArgSerTh	17		
150 ACACGCTGTCCGACAGCACACACAGCTGCCACTGCTCAGTTAGAAACAC	199		
17 rLysAspProCysProSerGlnProProValPheProAlaAlaLysGlnC	34		
200 AAAGGACCCCTGCGCCCTCCACGCCCCCACTGTTCCACAGCAGCTAAGCAT	249		
34 ysrProAlaLeuGluValThrTrpProGluValGluValProLeuasnGly	50		
250 GTCACACATGGAAAGAGACCTGACCACAGAGTGAAGTGCATGTAAATGA	299		
51 ThrLeuSerLeuSerCysValAlaCysSerArgPheProAsnPhSeril	67		
300 ACGCTAGAGCTTATCCTGCTGGCCCTGACAGCCGCTTCCCACTTAAGCAT	349		
67 eLeuTyrrTriPLeuGlyAsnGlySerPheIleGluHisLeuProGlyArgL	84		
350 CCTCTACTGTGCTGGGCAATGTTCTCTTATGTAGACACCTCCACAGCCGAC	399		
84 eutrPgluGlySerThrSerArgGluArgGlySerThrGlyThrGlnLeu	100		
400 TGTGGAGGGGAGCACACACCGGGAACGTGGGAGGACAGGTACGACGTG	449		
101 CysLysAlaLeuValLeuGluGlnLeuThrProAlaLeuHisSerThrAs	117		
450 TCGAAGGCTTGCTGCTGGAGCAGCTGACCCCTGCCCTGACACAGACCAA	499		
117 nPheSerCysValLeuValAspProGluGlnValValGlnArgHisValY	134		
500 CTTCCTCTGTGTGCTGTGGACCGTCGAACAGGTGTCCACAGCTCACGrCG	549		
134 alleuAlaGlnLeuThrPalaglyLeuArgAlaThrLeuProProThrGln	150		
550 TTCCTGCCACGCTGTGGGCTGTGAGGGCAACCTTCCCCCCCCACCAA	599		
151 GluAlaLeuProSerSerHisSerSerProGlnGlnGlnGly 164			
600 GAAGCCCTGCTCCACGACACAGCATGTCCACGACGACAGGGT 641			
seq_name: /SIDS1/gcdata/hold-geneseq/geneseqn-emb1/NA2000.DAT:AAA27384			
seq_documentation_block:			
ID AAA27384 standard; cDNA; 1356 BP.			
XX AAA27384;			
XX AC			
XX 16-AUG-2000 (first entry)			
XX DE			
XX Human IGFAM-4 immunoglobulin coding sequence.			
XX KW			
XX Human; Immunoglobulin; IGFAM-4; IGFAM; immune disorder; cancer;			
XX infection; inflammation; haematopoiesis; AIDS; allergy; ss.			
XX OS			
XX Homo sapiens.			
XX FH			
XX Key			
XX CDS			
XX Location/Qualifiers			
XX /tag= a			
XX /product= "IGFAM-4"			
XX sig_peptide			
XX /tag= b			
XX mat_peptide			
XX 242..673			

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FT      /*tag= c
PN      WO200029583-A2.
PD      25-MAY-2000.
XX
XX      19-NOV-1999; 99WO-US27566.
XX
XX      19-NOV-1998; 99US-0113635.
PR      22-DEC-1998; 98US-0113635.
PR      07-APR-1999; 99US-0128194.
XX
XX      (INCY-) INCYTE PHARM INC.
PI      Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;
PI      Lu DM, Lai P, Hillman JL, Yang J;
XX
XX      WPI: 2000-387796/73.
DR      P-PSDB: AAY96292.
XX
XX      Immunoglobulin superfamily proteins, the agonist and antagonist of the
PT      protein is useful for preventing and treating disorders associated with
PT      altered levels of the protein such as cancer, immune system disorders
PT      -
XX
XX      Claim 9; Page 96; 105pp; English.
XX
XX      The present sequence is the human immunoglobulin superfamily protein
CC      IGFAM-4 gene, which was isolated from a cDNA library of prostate tumour
CC      tissue. It is expressed in nervous, haematopoietic and immune and
CC      cardiovascular tissue, where cancer and inflammation are common. The
CC      gene, protein, its antibodies, agonists and antagonists are suitable for
CC      diagnosing and treating many diseases, including cancer, immune system
CC      disorders (such as inflammation, AIDS, allergies, anaemia,
CC      arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's
CC      disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,
CC      multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,
CC      systemic lupus erythematosus and ulcerative colitis), complications of
CC      cancer, haemodialysis and extracorporeal circulation, trauma and
CC      haematopoietic cancer (such as leukaemia) and infections caused by
CC      bacteria, viruses, fungi or parasites.
XX
XX      Sequence 1356 BP; 282 A; 458 C; 305 G; 311 T; 0 other:
SQ

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alignment_scores:
    Quality: 870.00      Length: 164
    Ratio: 5.305        Gaps: 0
    Percent Similarity: 100.000    Percent Identity: 100.000

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alignment_block:
US-09-786-130-1 x AAA27384 ..
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Align seg 1/1 to: AAA27384 from: 1 to: 1356
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1  ThrProValSerGlnThrThrThraAlaThrAlaSerValArgSerH 17
   |||||||
182 ACACCTGTCTGCAGACACACACAGCTGCACCTGCTGTTAGAGACAC 231
   |||||||
17  rLysAspProCysProSerGlnProProValPheProAlaAlaValSGLnc 34
   |||||||
232 AAAGAGCCCTGCTCCACGCCCACTGTTCCACAGAGCTAAGCACT 281
   |||||||
34  ySProAlaLeuGluValThrTrpProGluValGluValProLeuAsnGly 50
   |||||||
282 GTCCAGACATTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 331
   |||||||
51  ThrLeuSerLeuSerCysValAlaCysSerArgPheProAsnPheserH 67
   |||||||
332 AGCGTGAGCTTATCTGTGTGGCTGCACGCCCTTCCCACTTCAGCAT 381
   |||||||
67  eleuTyrrPleuGlyAsnGlySerPheIleGluHisLeuProGlyArgL 84
   |||||||

```

```

382 CCTCTACTGCTGGCGGCAAGTGCTTCATTATGAGCACTCCAGCCGAC 431
84  eutrpGluGlySerThrSerArgLuarGlySerThrGlyThrGlnLeu 100
   |||||||
432 TGTGGAGGGGAGACACAGCCGGGAAGTGTGGAGACAGGTACGACGCTG 481
   |||||||
101 CysLysAlaLeuValLeuGluGlnLeuThrProAlaLeuHisSerThrAs 117
   |||||||
482 TGCAGAGCCCTTGCTGTGGAGCAGTGCACCCCTGCTGCACAGACCAA 531
   |||||||
117 nPheSerCysValLeuValAspProGluGlnValAlaGlnArgHisValY 134
   |||||||
532 CTTCCTCTGTGCTGTGTGACCTGTACAGGTGTTCACAGCTGCG 581
   |||||||
134 alLeuAlaGlnLeuTrpAlaGlyLeuArgAlaThrLeuProProthrgln 150
   |||||||
582 TCCTGGCCCAAGCTCTGGGGCTGAGGGCAACCTTGCCCCCAACCAA 631
   |||||||
151 GluAlaLeuProSerSerHisSerSerProGlnGlnGly 164
   |||||||
632 GAAGCCCTGCTGCACAGCACACAGCTCCACACAGCAGAGGT 673
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seq_name: /SIDSL/gcdata/hold-geneseq/geneseqn-emb1/NA1999.DAT:AAx24751
seq_documentation_block:
ID  AAx24751 standard; cDNA: 7063 BP.
XX
XX  AAx24751:
XX
XX  21-JUN-1999 (first entry)
XX
DE  Human interleukin-18 binding protein splice variant IL-18Bpc cDNA.
XX
XX  Interleukin-18 binding protein; IL-18BP; IL-18Bpc; splice variant;
KW  human; autoimmune disease; inflammation; diabetes; pancreatitis;
KW  rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis;
KW  psoriasis; inflammatory bowel disease; multiple sclerosis;
KW  ischemic heart disease; ischemic brain injury; gene therapy; ss.
XX
XX  Homo sapiens.
XX
XX  Key  location/Qualifiers
FH  949..1542
FT  CDS
FT  /*tag= a
FT  /product= "IL-18Bpc"
FT  sig_peptide 949..1032
FT  /*tag= b
FT  mat_peptide 1033..1539
FT  /*tag= c
XX
XX  WO9909063-A1.
XX
XX  25-FEB-1999.
XX
XX  13-AUG-1998; 98WO-IL00379.
XX
XX  22-JUL-1998; 98IL-0125463.
PR  14-AUG-1997; 97IL-0121554.
PR  27-AUG-1997; 97IL-0121639.
PR  29-SEP-1997; 97IL-0121860.
PR  06-NOV-1997; 97IL-0122134.
XX
XX  (YEDA ) YEDA RES & DEV CO LTD.
XX
XX  DiNarello C, Kim SH, Novick D, Rubinstein M;
PI  WPI: 1999-180975/15.
XX
XX  P-PSDB: AAM96006.
XX
XX  New interleukin-18 binding protein - useful for treating human
PT  diseases, including autoimmune disease and inflammation
PT
XX
XX  Claim 12; Page 55-58; 100pp; English.
PS

```

XX The present sequence represents a cDNA clone coding for a human
 CC interleukin-18 binding protein (IL-18BP) splice variant designated
 CC IL-18BPc (see AAW98006). This is one of 4 novel splice variants (see
 CC AAX24749-52), all coding for putative soluble proteins (see
 CC AAW98004-07), that were detected following a screening of human
 CC peripheral blood monocyte, Jurkat T-cell, peripheral blood
 CC mononuclear cell and spleen cell cDNA libraries using a probe
 CC produced using IL-18BP-specific primers. IL-18BPc is a low
 CC abundance splice variant. IL-18BP polypeptides capable of
 CC binding IL-18 and/or modulating and/or blocking IL-18 activity are
 CC provided. Methods for their isolation and recombinant production,
 CC DNA vectors expressing them, vectors useful for their expression in
 CC humans and other mammals, and antibodies against them are also
 CC provided. IL-18BP polypeptides, and DNA encoding them, can be used
 CC to treat conditions requiring the protein (claimed). Conditions
 CC include autoimmune diseases, type I diabetes, rheumatoid arthritis,
 CC graft rejections, inflammatory bowel disease, sepsis, multiple
 CC sclerosis, ischemic heart diseases, ischemic brain injury, chronic
 CC hepatitis, psoriasis, and chronic/acute pancreatitis. IL-18BP is
 CC also useful for purifying IL-18 (claimed).

XX Sequence 7063 BP, 1538 A; 2025 C; 1981 G; 1519 T; 0 other;

alignment_scores:

Quality: 821.50 Length: 241
 Ratio: 5.009 Gaps: 1
 Percent Similarity: 68.050 Percent Identity: 68.050

alignment_block:

US-09-786-130-1 x AAX24751 ..

Align seg 1/1 to: AAX24751 from: 1 to: 7063

1 ThrProValSerGlnThrThrAlaAlaThrAlaSerValArgSerTh 17
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 1033 ACACCTGTCTCGACAGACCACACAGCTGCCCTCCTCAGTTAGAGAC 1082
 17 rlyAspProCysProSerGlnProProValPheProAlaAlaLysGlnC 34
 |||||||
 1083 AAGAGACCCCTGGCCCTCCAGCCCGCCAGTCTCCAGCAGCTAAGAGCT 1132
 34 ySProAlaLeuGluValThrTrpProGluValGluValProLeuAsnGly 50
 |||||||
 1133 GTCCAGCATTTGGAAGTGAACCTGGCCAGAGGTGGAGTCCCACTAATGGA 1182
 51 ThrLeuSerLeuSerCysValAlaCysSerArgPheProAsnPhSer11 67
 |||||||
 1183 ACCTGTAGCTTATCTGTGTGGCTTGCAGCCGCTTCCCAACTTCACGAT 1232
 67 eleuTyTrpLeuGlyAsnGlySerPheIleGluHisLeuProGlyArgL 84
 |||||||
 1233 CCTTCTACTGTGGGCAATGTCTTCATTTGACACCTCCAGGCGGAC 1282
 84 euTrpGluGlySerThrSerArgGluArgGlySerThrGlyThrGluLeu 100
 |||||||
 1283 TTGTGGAGGGGAGACACCGCGGGAAGCTGGGAGACACAGATGCCACTG 1332
 101 CysLysAlaLeuValLeuGluGlnLeuThrProAlaLeuHisSerThas 117
 |||||||
 1333 TGCAGAGCCTTGTGGCTGGAGCAGCTGACCCCTCCCTGCACACACACAA 1382
 117 nPhSerCysValLeuValAspProGluGlnValValGlaArgHisValy 134
 |||||||
 1383 CTTCCTCTGTGTCTGTGGACCTTGAAACAGGTGTCCACGCTACGCTGG 1432
 134 alleuAlaGlnLeuTrp..... 139
 |||||||
 1433 TCTGTGGCCCAAGCTCTGGGTGAGGAGCCCAAGAGAGGCTCCAGAAACAG 1482
 139 139

1483 GAGGAGCTCTGCTTCCATATGTGGGAGGAAAGGTGGCTCTGCCAGAG 1532
 139 139
 1533 CAGCTGTGAACATAATGCCACAGCATCTCTCAAGGTACACGACAAAAAG 1582
 139 139
 1583 GAACCTAGTCTTGGGACAGAGAGGTAGCCTGGGGCAAGTATGAGA 1632
 140 A1 140
 1633 TGCTCCCTCTTCTCTTGGCCGATTCCTGTCTGCTTCACTTCCCTAGGC 1682
 140 aglyLeuArgAlaThrLeuProThrGlnGluValLeuProSerSerH 157
 |||||||
 1683 TGGCTGAGGGCAACCTTGGCCCCCACCACCAAGAACCTTGGCTTCACGCC 1732
 157 isSerSerProGlnGlnGlnGly 164
 |||||||
 1733 ACAGCAGTCCACAGCAGCAGGCT 1755

seq_name: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT:AA11004

seq_documentation_block:

ID AA11004 standard; DNA; 411 BP.

AC AA11004;

DT 28-JUL-2000 (first entry)

DE Human IL-18 binding protein 5' RACE fragment #1.

KW Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
 KW regulator; drug; sensitivity disease; organ rejection; organ transplant;
 KW autoimmune disease; rapid amplification of cDNA ends; RACE; ss.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 1..411

FT *tag- a

FT /partial

FT /note="fragment of N-terminus of IL-18 binding protein"

PN WO200012555-A1.

PD 09-MAR-2000.

PF 18-NOV-1998; 98WO-JP05186.

PR 01-SEP-1998; 98JP-0247588.

PR 18-NOV-1998; 98JP-0327914.

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

PI Torigoe K, Tanai M, Kurimoto M;

DR WPI; 2000-237850/20.

DR P-PSDB; AAY83982.

PT Interleukin 18-binding protein with activity of regulating
 PT physiological actions of interleukin 18, useful as regulator and drug
 PT for sensitivity diseases and organ rejection and in treating diseases
 PT due to excess immune reaction

PS Example 2; Page 60-61; 71pp; Japanese.

CC The invention relates to novel interleukin 18 (IL-18)-binding proteins
 CC from humans or mice which act as regulators and drugs for sensitivity
 CC diseases and organ rejection and in treating diseases due to excess
 CC immune reaction, e.g. in slowing down rejection after organ transplant,
 CC and in treating autoimmune diseases. This sequence represents the initial

CC fragment isolated by a 5' RACE (Rapid Amplification of cDNA Ends)
 CC reaction for the 5' end of the interleukin 12 binding protein coding
 CC sequence.

XX Sequence 411 BP; 81 A; 138 C; 114 G; 78 T; 0 other;

alignment_scores:

Quality: 727.00 Length: 137
 Ratio: 5.307 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-786-130-1 x AAX11004 ..

Align seg 1/1 to: AAX11004 from: 1 to: 411

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1 ThrProValSerGlnThrThrAlaAlaThrAlaSerValArgSerth 17
  |||
1 AACACCTGCTCGACACACACACAGCTGCCTCAGTTCAGTGAAGCAC 50
  |||
17 rlysaAPProCysProSerGlnProProValPheProAlaAlaLysGlnC 34
  |||
51 AAGAGACCCCTGCCCCCTCCAGCCCCAGGTTCACAGCAGCTAAGCAGT 100
  |||
34 ySPRoAlaLeuGluValThrTrpProGluValGluValProLeuAangly 50
  |||
101 GTCCAGCATTTGGAGTAGCTGACCTGGCCAGAGGTGAAGTGCACAGTAAGGA 150
  |||
51 ThrLeuSerLeuSerCysValAlaCysSerArgPheProAsnPheSeril 67
  |||
151 AGCGTAGCTATTCGTGTGGCTGCACCGCTTCCCACTTCAGCAT 200
  |||
67 eleuTyrrPLeuGlyAsnGlySerPheIleGluHisLeuProGlyArgL 84
  |||
201 CCTTACTGTGGTGGCAATGTTCTTCATTGAGCAGCTCCAGGCGCGAC 250
  |||
84 euTrpGluGlySerThrSerArgGluArgGlySerThrGlyhrGlnLeu 100
  |||
251 TGTGGAGGGGAGACACACCGGAACTGGGAGCAGAGTACGCACTG 300
  |||
101 CysLysAlaLeuValLeuGluGlnLeuThrProAlaLeuHisSerThras 117
  |||
301 TGCAGAGCCTTGTGCTGAGCAGCTGACCCCTGCGCTCAGACAGCA 350
  |||
117 nPheSerCysValLeuValAspProGluGlnValValGlnArgHisValy 134
  |||
351 CTTCCTCTGCTGTGCTGTGGACCTGAAACAGCTGTCCAGCGTCAGCTCG 400
  |||
134 alleuAlaGln 137
  |||
401 TCCGTGGCCGAG 411
  |||
seq_name: /SIDS1/gcdata/hold-geneseq/geneseqn-emb1/NA11999.DAT: AAX24753
seq_documentation_block:
ID AAX24753 standard; cDNA; 7812 BP.
XX
AC AAX24753;
XX
DT 21-JUN-1999 (first entry)
XX
DE Human interleukin-18 binding protein gene.
XX
KW Interleukin-18 binding protein; IL-18BP; IL-18BPd; splice variant;
KW human; autoimmune disease; inflammation; diabetes; pancreatitis;
KW rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis;
KW psoriasis; inflammatory bowel disease; multiple sclerosis;
KW ischemic heart disease; ischemic brain injury; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN M09909063-A1.
```

XX 25-FEB-1999.

XX 13-AUG-1998; 98WO-IL00379.

XX 22-JUL-1998; 98IL-0125463.

XX 14-AUG-1997; 97IL-0121564.

XX 27-AUG-1997; 97IL-0121639.

XX 29-SEP-1997; 97IL-0121860.

XX 06-NOV-1997; 97IL-0122134.

XX (YEDA) YEDA RES & DEV CO LTD.

XX Diarello C, Kim SH, Novick D, Rudinstein M;

XX WPI; 1999-180975/15.

XX New interleukin-18 binding protein - useful for treating human

XX diseases, including autoimmune disease and inflammation

XX Disclosure; Page 60-63; 100pp; English.

XX The present sequence comprises human interleukin-18 binding protein

XX (IL-18BP) genomic DNA. It was produced from 5 genomic clones

XX isolated from a human genomic library by screening with full-length

XX human IL-18BP cDNA. No exon coding for a transmembrane receptor

XX was identified within the 7.8 kb sequence. 4 Splice variant clones

XX (see AAX24749-52) were identified that code for putative soluble

XX secreted proteins, designated IL-18BPa-d (see AA98004-007). The

XX IL-18BP locus contains an additional gene, coding for the nuclear

XX mitotic apparatus protein 1 (NUMA1), positioned on the minus strand.

XX This localised the IL-18BP gene to human chromosome 11q13(36).

XX IL-18BP polypeptides capable of binding IL-18 and/or modulating

XX and/or blocking IL-18 activity are provided by the invention.

XX Methods for their isolation and recombinant production, DNA vectors

XX expressing them, vectors useful for their expression in humans and

XX other mammals, and antibodies against them are also provided.

XX IL-18BP polypeptides, and DNA encoding them, can be used to treat

XX conditions requiring the protein (claimed). Such conditions

XX include autoimmune diseases, type I diabetes, rheumatoid arthritis,

XX graft rejections, inflammatory bowel disease, sepsis, multiple

XX sclerosis, ischemic heart diseases, ischemic brain injury, chronic

XX hepatitis, psoriasis, and chronic/acute pancreatitis. IL-18BP is

XX also useful for purifying IL-18 (claimed).

XX Sequence 7812 BP; 1689 A; 2278 C; 2167 G; 1678 T; 0 other;

alignment_scores:

Quality: 638.50 Length: 483
 Ratio: 3.893 Gaps: 5
 Percent Similarity: 33.954 Percent Identity: 33.540

alignment_block:

US-09-786-130-1 x AAX24753 ..

Align seg 1/1 to: AAX24753 from: 1 to: 7812

```

1 ThrProValSerGlnThrThrAlaAlaThrAlaSerValArgSerth 17
  |||
1105 AACACCTGCTCGACACACACACAGCTGCCTCAGTTCAGTGAAGCAC 1154
  |||
17 rlysaAPProCysProSerGlnProProValPheProAlaAlaLysGlnC 34
  |||
1155 AAGAGACCCCTGCCCCCTCCAGCCCCAGGTTCACAGCAGCTAAGCAGT 1204
  |||
34 ySPRoAlaLeuGluValThrTrpProGluValGluValProLeu..... 48
  |||
1205 GTCCAGCATTTGGAGTAGCTGACCTGGCCAGAGGTGAAGTGCACAGTAA 1254
  |||
48 ..... 48
1255 AAGCAGAGTGTGAGGGTGTGCTATGGGACACAGAGTTCCAGGCTGCG 1304
```

```
48 ..... 48
1305 GTTACTCTGAGCCAGTCCCTTCTGCCCATTGACACCACTGAGC 1354
48 ..... 48
1355 CAGCTGGGCTGAGCAGCAGCACTTCTCCCTCCCAACCCAGTGTGAGG 1404
48 ..... 48
1405 TGCAGGCTTGGCGAGCTCCCAAGATGCTCCCTATCAATAGACAGAGA 1454
48 ..... 48
1455 ACTAAGACATAAGTAATGTCACAGACCTCCAGAGCTTGGTTGCAG 1504
48 ..... 48
1505 TGAACCCCAAGGCCAGCCCTCCACCCAGAGCCTGTGGCCTGTGGCAT 1554
48 ..... 48
1555 CTCAGAGAGCAGCAGCCATCCAGCAGCTGCTCTGTCACCTGGGCTCCA 1604
48 ..... 48
1605 AGTACCCGAGGCTGGCAGCTAGAAAAGTCTCTCTGAGGAGACAGTTCA 1654
48 ..... 48
1655 GAAAGAGATTATCATCGTAGAACCAAGACATTCCTCATTCCCGGTGT 1704
48 ..... 48
1705 TTAAGGCTAGGGCCTCTCGAGACACTGCATTCTGTAAAGGAGAGTTC 1754
48 ..... 48
1755 CACCTAGTGTGTGCAGAGCAGATTCTCTAGGTTCCAGATGCAATGGGAC 1804
48 ..... 48
1805 TGGGGGAGCTGGCAGAGAGGGCAGACAGAGCAGAGGTAGGGGAAGGCC 1854
49 ..... Asn..GlyThrLeu 53
1855 TGCTCTTCTGAAGAGCTAACTGCTGCTGTGCTCCCTAGATGGAAAGCTGA 1904
53 erLeuSerCysValAlaCysSerArpPheProAsnPheSerIleLeuTyr 69
1905 GCTTATCTGTGTGCTGCGAGCGGCTTCCCACTTCAGATCTCTCTAC 1954
70 TrpLeuGlnAsnGlySerPheIleGlnHisLeuProGlyArgLeuTrpG1 86
1955 TGGCTGGGCAATGCTCTTCATTGAGCACCCTCCAGGCGCAGCTGTGGGA 2004
86 uGly..... 87
2005 GGGGAGCAACAGGTGAGGGTCCGACAGCAAGGTGGGTGGGAAGAAACC 2054
88 ..... Ser..ThrSerArgLys 93
2055 TTCTGGGGCTTCTCATGACCTTTCCTCCCTGCTCCAGCGGGAGAC 2104
93 rglGlySerThrGlyThrGlnLeuCysLysAlaLeuValLeuGlnLeu 109
2105 GTGGGACACAGGTACGAGCTGTGCAAGGCTTGTGCTGAGACACACTG 2154
110 ThrProAlaLeuHisSerThrAsnPheSerCysValLeuValaLappProG1 126
2155 ACCCTGCTCCGACAGCAGCAACTTCTCTGTGTGCTGTGAGACCTGA 2204
```

```
126 uGlnValValGlnArgHisValIleuAlaGlnLeuTrp..... 139
|||||
2205 ACAGGTTGTCAGCGCTCACGTGCTGCTGCCCCAGCTGTGGGAGAGACC 2254
139 ..... 139
2255 CAAGAGAGGCGCTCCAGAGACAGAGAGAGCTGTGCTTCATATGTGGGGA 2304
139 ..... 139
2305 GGAAGGCTGGGCTCTGCCAGAGCAGCCTGTGAATAATGCCACATTC 2354
139 ..... 139
2355 CTCAGGTACACCAACAAAAAGACTTAGTCTTGGCGAGAGAGGTG 2404
139 ..... 139
2405 TAGCCTGGGCAAGTGAATGATGTCCCTCTTCTTGGCGTATCCT 2454
140 ..... AlaglyLeuArgAlaThrLeuProProth 149
2455 TGCTGCTTCACCTTCCTCCTAGGCTGGGCTGAGGCAACCTTGGCCCGAC 2504
149 rGlnGlnAlaLeuProSerSerHisSerSerProGlnGlnGly 164
|||||
2505 CCAAGAAAGCCCTGCTCCAGCCACAGCAGTCCACAGCAGCAGGCT 2550
seq_name: /SIDSI/gcgdata/hold-geneseq/geneseq-n-emb1/NA1999.DAT:AAx24752
seq_documentation_block:
ID AAX24752 standard; cDNA; 1360 BP.
XX
AC AAX24752;
XX
DT 21-JUN-1999 (first entry)
XX
DE Human Interleukin-18 binding protein splice variant IL-18Bpd cDNA.
XX
KW Interleukin-18 binding protein; IL-18BP; IL-18Bpd; splice variant;
KW human; autoimmune disease; inflammation; diabetes; pancreatitis;
KW rheumatoid arthritis; graft rejection; sepsis; chronic hepatitis;
KW psoriasis; inflammatory bowel disease; multiple sclerosis;
KW ischemic heart disease; ischemic brain injury; gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Location/Qualifiers
FT CDS 169..654
FT FT /*tag= a
FT FT /product= "IL-18Bpd"
FT sig_peptide 169..252
FT FT /*tag= b
FT mat_peptide 253..651
FT FT /*tag= c
XX
PN MO9909063-A1.
XX
PD 25-FEB-1999.
XX
PF 13-AUG-1998; 98WO-IL00379.
XX
PR 22-JUL-1998; 98IL-0125463.
PR 14-AUG-1997; 97IL-0121554.
PR 27-AUG-1997; 97IL-0121639.
PR 29-SEP-1997; 97IL-0121860.
PR 06-NOV-1997; 97IL-0122134.
XX
PA (YEDA ) YEDA RES & DEV CO LTD.
XX
PI dinarello C, kim SH, Novick D, Rubinstein M;
XX
WP1; 1999-180975/15.
```

DR P-PSDB: AAW98007.

XX New interleukin-18 binding protein - useful for treating human
PT diseases, including autoimmune disease and inflammation
XX

PS Claim 12; Page 59; 100pp; English.

XX The present sequence represents a cDNA clone coding for a human
CC interleukin-18 binding protein (IL-18BP) splice variant designated
CC IL-18Bpd (see AAW98007). This is one of 4 novel splice variants (see
CC AAX24749-52), all coding for putative soluble proteins (see
CC AAW98004-07), that were detected following a screening of human
CC peripheral blood monocyte, Jurkat T-cell, peripheral blood
CC mononuclear cell and spleen cell cDNA libraries using a probe
CC produced using IL-18BP-specific primers. IL-18Bpd is a low
CC abundance splice variant. IL-18BP polypeptides capable of
CC binding IL-18 and/or modulating and/or blocking IL-18 activity are
CC provided. Methods for their isolation and recombinant production,
CC DNA vectors expressing them, vectors useful for their expression in
CC humans and other mammals, and antibodies against them are also
CC provided. IL-18BP polypeptides, and DNA encoding them, can be used
CC to treat conditions requiring the protein (claimed). Conditions
CC include autoimmune diseases, type I diabetes, rheumatoid arthritis,
CC graft rejections, inflammatory bowel disease, sepsis, multiple
CC sclerosis, ischemic heart diseases, ischemic brain injury, chronic
CC hepatitis, psoriasis, and chronic/acute pancreatitis. IL-18BP is
CC also useful for purifying IL-18 (claimed).

XX Sequence 1360 BP; 289 A; 454 C; 303 G; 314 T; 0 other;

alignment_scores:

Quality: 598.50 Length: 165
Ratio: 4.946 Gaps: 2
Percent Similarity: 73.333 Percent Identity: 72.727

alignment_block:

US-09-786-130-1 x AAX24752 ..

Align seg 1/1 to: AAX24752 from: 1 to: 1360

1 ThrProValSerGlnThrThrAlaAlaThrAlaSerValArgSerTh 17
|||||
253 ACACCTGTCTGCGACACACAGCTGCCAGCTCTCGTGAAGAGCACC 302
17 rlysaSPProCysProSerGlnProProValPheProAlaAlaLysGlnC 34
|||||
303 AAAGGACCCCTGCGCTCCAGCCGCCAGTGTCCAGCAGCAAGCAACT 352
34 yPrProAlaLeuGlnValThrTrpProGlnValGlnValProLeuAsnGly 50
|||||
353 GTCCAGCATTTGGAGTGAAGTCCGCGAGAGTGGAAAGTGCACATGGA 402
51 ThrLeuSerLeuSerCysValAlaCysSerArgPheProAsnPheSerIl 67
|||||
403 AGCGTAGCTTATCCTGTGCTGCGCTGACGCCCTTCCCAACTTCCAGCAT 452
67 eleuTyTrPLeuGlyAsnGlySerPheIleGlnIleuProGlnLysGln 84
|||||
453 CCTTACTGTGGTGGCAATGTTCTTATGAGCACTCCAGGCGGCAC 502
84 eUTrGlnGlySerThrSerArgGlnArgGlySerThrGlnThrGlnLeu 100
|||||
503 TGTGGAGGAGGAGCAGCAGCCGGAACSTGGGAGCACA..... 540
101 CysLysAlaLeuValLeuGlnLeuThrProAlaLeuHisSerThrAs 117
540 540
117 rPheSerCysValLeuValAspProGlnGlnValGlnArgHisVal 134
540 540

134 alleuAlaGlnLeuTrpAla.GlyLeuArgAlaThrLeuProThrGln 150
541GGCTGGGCTGAGGGCAACCTGCCCCCAACCA 573
150 ngIuAlaLeuProSerSerHisSerSerProGlnGlnGly 164
574 AGAAGCCCTGCTCCAGCCAGCAGCATCCACAGCAGCAGGCT 616

seq_name: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT:AAA11003

seq_documentation_block:

ID AAA11003 standard; DNA; 495 BP.

XX AAA11003;

DT 28-JUL-2000 (first entry)

DE Mouse mature interleukin 18 binding protein coding sequence.

XX Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
KW regulator; drug; sensitivity disease; organ rejection; organ transplant;
KW autoimmune disease; ss.

OS Mus musculus.

PN WO200012555-A1.

PD 09-MAR-2000.

PF 18-NOV-1998; 98WO-JP05186.

XX 01-SEP-1998; 98JP-0247588.

PR 18-NOV-1998; 98JP-0327914.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

PI Toriogue K, Taniai M, Kurimoto M;

XX WPI; 2000-237850/20.

PT Interleukin 18-binding protein with activity of regulating
PT physiological actions of interleukin 18, useful as regulator and drug
PT for sensitivity diseases and organ rejection and in treating diseases
PT due to excess immune reaction

PS Claim 6; Page 57-59; 71pp; Japanese.

CC The invention relates to novel interleukin 18 (IL-18)-binding proteins
CC from humans or mice which act as regulators and drugs for sensitivity
CC diseases and organ rejection and in treating diseases due to excess
CC immune reaction, e.g. in slowing down rejection after organ transplant,
CC and in treating autoimmune diseases. This sequence represents the
CC coding sequence for the mature mouse interleukin 12 binding protein.

XX Sequence 495 BP; 117 A; 156 C; 116 G; 106 T; 0 other;

alignment_scores:

Quality: 515.00 Length: 158
Ratio: 3.902 Gaps: 3
Percent Similarity: 83.544 Percent Identity: 66.456

alignment_block:

US-09-786-130-1 x AAA11003 ..

Align seg 1/1 to: AAA11003 from: 1 to: 495

1 ThrProValSerGlnThrThrAlaAlaThrAlaSerValArgSerTh 17
||| :|||
1 ACATGTCACCTCAGACAACT.....GCCACTGTCTTAACTGAAGATC 44
17 rlysaSPProCysProSerGlnProProValPheProAlaAlaLysGlnC 34
:||||| ||| :|||


```
45 AAAAGACCATCTCTCTGCTCCAGCAGTCCA...ACTAAGCAGT 91
34 yspProAlaLeuGluValThrTriProGluValProLeuAsnGly 50
   |||||.....||| ||||| |||||.....|||
92 ACCAGACACTGATGATTTGGCCAAAAAGAGTCCACTGAATGA 141
51 ThrLeuSerLeuSerCysValAlaCysSerArgPheProAsnPheSer11 67
   |||||.....||| ||||| |||||.....|||
142 ACTGTGACCTGTGCTGCTACTGCTGCAGCGCTTCCCTACTTCACCAT 191
67 eLeuTYTriPLeuGlyAsnGlySerPheIleGluHisLeuProGlyArgL 84
   |||||.....||| ||||| |||||.....|||
192 CCTTACTGCTGGCGCAATGCTTCTTCATTGACACCTTCAGGCGGCG 241
84 eutRPGluGlySerThrSerArgGluArgGlySerThrGlyThrGlnLeu 100
   || ||||| |||||.....||| |||||.....|||
242 TGAAGGAGGGCCACACAAAGTCGCGAGCAGACAGACACAGACCTGCTG 291
101 CysLysAlaLeuValLeuGluGlnLeuThrProAlaLeuHisSerThrAs 117
   ::|||.....||| ||||| |||||.....|||
292 CACAGGCGCTTGGTGGTGAAGAACTGAGCCGCCCTAGAGAGTACCAA 341
117 nPheSerCysValLeuValAspProGluGlnValAlaGlnArgHisValY 134
   |||||.....||| ||||| |||||.....|||
342 CTTCTCTGCTGTTGTGTGTGATCTGACAAAGTGGCCACTATCACATCA 391
134 alleuAlaGlnLeuTriPAlaGlyLeuArgAlaThrLeuProProThrGln 150
   ::|||.....||| ||||| |||||.....|||
392 TTCTGGCCGCGCTCTGGGATGGGTTGAAGACAGCTCCGCTTCTCAAA 441
151 GluAlaLeuProSerSerHisSer 158
   |||::||| |||||.....|||
442 GAAACCTC...TCTAGCCACAGC 462

seq_name: /SID1/gcgdata/hold-geneseq/geneseq-emb1/NA2000.DAT:AAA11011
seq_documentation_block:
ID AAA11011 standard; DNA; 847 BP.
XX
AC AAA11011;
XX
DT 28-JUL-2000 (first entry)
XX
DE Mouse interleukin 18 binding protein complete coding sequence.
XX
KM Immunosuppressant: interleukin 18 binding protein; IL18-BP; human; mouse;
KM regulator; drug; sensitivity disease; organ rejection; organ transplant;
KM autoimmune disease; ds.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 151..732
   /*tag= a
FT sig_peptide /product= "mouse interleukin 18 binding protein"
   /*tag= b
FT mat_peptide 235..729
   /*tag= c
XX
PN WO200012555-A1.
XX
PD 09-MAR-2000.
XX
PF 18-NOV-1998; 98WO-JP05186.
XX
PR 01-SEP-1998; 98JP-0247588.
PR 18-NOV-1998; 98JP-0327914.
XX
PA (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI Torioge K, Taniiai M, Kurimoto M;
XX
```

```
DR WPI: 2000-237850/20.
DR P-PSDB: AAY83989.
XX
PT Interleukin 18-binding protein with activity of regulating
PT physiological actions of interleukin 18, useful as regulator and drug
PT for sensitivity diseases and organ rejection and in treating diseases
PT due to excess immune reaction
XX
PS Example 4; Page 67-69; 71pp; Japanese.
XX
CC The invention relates to novel interleukin 18 (IL-18)-binding proteins
CC from humans or mice which act as regulators and drugs for sensitivity
CC diseases and organ rejection and in treating diseases due to excess
CC immune reaction, e.g. in slowing down rejection after organ transplant,
CC and in treating autoimmune diseases. This sequence represents the coding
CC sequence for the full length mouse interleukin 12 binding protein.
XX
SQ Sequence 847 BP; 198 A; 257 C; 205 G; 187 T; 0 other;

alignment_scores:
   Quality: 515.00 Length: 158
   Ratio: 3.902 Gaps: 3
   Percent Similarity: 83.544 Percent Identity: 66.456

alignment_block:
US-09-786-130-1 x AAA11011 ..

Align seg 1/1 to: AAA11011 from: 1 to: 847

1 ThrProAlaSerGlnThrThrAlaAlaThrAlaSerValArgSerTh 17
   ||| ::| ||||| |||||::| ::| |||
235 ACATCTGCACCTCAGACACT.....GCCACTGTCTTAAGTGAACCTC 278
17 rLysAspProCysProSerGlnProProValPheProAlaAlaLysGlnC 34
   :|||.....||| |||::| |||
279 AAAAGACCATGCTCTCTGCTCCAGCAGTCCA...ACTAAGCAGT 325
34 yspProAlaLeuGluValThrTriProGluValGluValProLeuAsnGly 50
   |||||.....||| ||||| |||||.....|||
326 ACCAGCACTGATGATTTGGCCAGAAAAAGAGTCCACTGAATGA 375
51 ThrLeuSerLeuSerCysValAlaCysSerArgPheProAsnPheSer11 67
   |||||.....||| ||||| |||||.....|||
376 ACTCTGACCTGTGCTGCTACTGCTGCAGCGCTTCCCTACTTCACCAT 425
67 eLeuTYTriPLeuGlyAsnGlySerPheIleGluHisLeuProGlyArgL 84
   |||||.....||| ||||| |||||.....|||
426 CTTCTACTGCTGGCGCAATGCTTCTTCATTGAGCACCTTCAGGCGGCG 475
84 eutRPGluGlySerThrSerArgGluArgGlySerThrGlyThrGlnLeu 100
   || ||||| |||||.....||| |||||.....|||
476 TGAAGGAGGGCCACACAAAGTCGCGAGCAGACAGACACAGACCTGCTG 525
101 CysLysAlaLeuValLeuGluGlnLeuThrProAlaLeuHisSerThrAs 117
   ::|||.....||| ||||| |||||.....|||
526 CACAGGCGCTTGGTGGTGAAGAACTGAGCCGCCCTAGAGAGTACCAA 575
117 nPheSerCysValLeuValAspProGluGlnValAlaGlnArgHisValY 134
   |||||.....||| ||||| |||||.....|||
576 CTTCTCTGCTGTTGTGTGTGATCTGACAAAGTGGCCACTATCACATCA 625
134 alleuAlaGlnLeuTriPAlaGlyLeuArgAlaThrLeuProProThrGln 150
   ::|||.....||| ||||| |||||.....|||
626 TTCTGGCCGCGCTCTGGGATGGGTTGAAGACAGCTCCGCTTCTCAAA 675
151 GluAlaLeuProSerSerHisSer 158
   |||::||| |||||.....|||
676 GAAACCTC...TCTAGCCACAGC 696

seq_name: /SID1/gcgdata/hold-geneseq/geneseq-emb1/NA2000.DAT:AAA11008
seq_documentation_block:
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```

ID   AAA11008 standard; DNA; 351 BP.
XX
AC   AAA11008;
XX
DT   28-JUL-2000 (first entry)
XX
DE   Mouse IL-18 binding protein 5' RACE fragment #1.
XX
KW   Immunosuppressant; interleukin 18 binding protein; IL18-BP; human; mouse;
KW   regulator; drug; sensitivity disease; organ rejection; organ transplant;
KW   autoimmune disease; rapid amplification of cDNA ends; RACE; ss.
XX
OS   Mus musculus.
XX
FH   Key      Location/Qualifiers
FT   CDS      1..351
FT             /tag=a
FT             /partial
FT             /note="fragment of N-terminus of IL-18 binding protein"
XX
PN   WO200012555-A1.
XX
PD   09-MAR-2000.
XX
PF   18-NOV-1998; 98WO-JP05186.
XX
PR   01-SEP-1998; 98JP-0247588.
PR   18-NOV-1998; 98JP-0327914.
XX
PA   (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI   Torigoe K, Tanai M, Kurimoto M;
XX
DR   WPI: 2000-237850/20.
DR   P-FSDB; AAY83986.
XX
PT   Interleukin 18-binding protein with activity of regulating
PT   physiological actions of interleukin 18, useful as regulator and drug
PT   for sensitivity diseases and organ rejection and in treating diseases
PT   due to excess immune reaction
XX
PS   Example 4; Page 65; 71pp; Japanese.
XX
SS   The invention relates to novel interleukin 18 (IL-18)-binding proteins
SS   from humans or mice which act as regulators and drugs for sensitivity
SS   diseases and organ rejection and in treating diseases due to excess
SS   immune reaction, e.g. in slowing down rejection after organ transplant,
SS   and in treating autoimmune diseases. This sequence represents the initial
SS   fragment isolated by a 5' RACE (Rapid Amplification of cDNA Ends)
SS   reaction for the 5' end of the mouse interleukin 12 binding protein
SS   coding sequence.
XX
SQ   Sequence 351 BP; 82 A; 103 C; 90 G; 76 T; 0 other;

```

```

alignment_scores:
  Quality: 441.00      Length: 112
  Ratio: 4.410        Gaps: 0
  Percent Similarity: 89.286  Percent Identity: 74.107

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alignment_block:
  US-09-786-130-1 x AAA11008

```

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Align seg 1/1 to: AAA11008 from: 1 to: 351
32 LysGInCysProAlaLeuGluValThrTrpProGluValGluValProLeu 48
13 AAGCAGTACCCGACGACGTGATGTGATGGCCAGAAAAAGAGTGCACACT 62
48 uasnlythrleuSerleuSerCysValAlaLacySerArgpneProasnP 65
63 GAATGAACTCTGACCTTGTCTGTACTGACGCGGACGCGCTTCCCTACT 112

```

```

65 heserlleuTrpTrpLeuGlyAsnGlySerPheIleGluHisLeuPro 81
113 TCACATCCTCTACTGCTGGCAATGTTCTTCATTGAGACCTTCCA 162
82 GlyArgLeuTrpGluGlySerThrSerArgGluArgGlySerPheGlyTh 98
163 GCGCGGCTGAAGGAGGCGCACACAGTCGCGAGCAGACGAAACACAC 212
98 rGlnLeuCysLysAlaLeuValLeuGluGlnLeuThrProAlaLeuHis 115
213 CTGGCTGCACAGGCGCTTGTGCTGCGAAGAACTGAGCCACCTACGAA 262
115 erThraspneserCysValLeuValAspProGluGlnValGlnArg 131
263 GTACCAACTTCTCTCTGTTGTTGTTGATCTGACAACTGCGCCACTAR 312
132 HisValValLeuAlaGlnLeuTrpAlaGlyLeuArg 143
313 CACATCTTCTGGCCCGCCAGCTCTGGATGGCTTGAG 348

seq_name: /SIDS1/gcgcdata/hold-geneseq/genesegn-emb1/NA2000.DAT:AAA43451
seq_documentation_block:
ID   AAA43451 standard; cDNA; 495 BP.
XX
AC   AAA43451;
XX
DT   21-AUG-2000 (first entry)
XX
DE   Mouse secreted expressed sequence tag SEQ ID NO:26.
XX
KW   Human; mouse; chicken; rat; secreted expressed sequence tag; SEST;
KW   expressed sequence tag; EST; probe; chemotactic; proliferative;
KW   immunomodulatory; haemopoietic; chemokinetic; analgesic; haemostatic;
KW   thrombolytic; antiinflammatory; cyostatic; antibacterial; antifungal;
KW   antiviral; antidiabetic; antisthmatic; vulnerrary; antiparkinsonian;
KW   antitumor; osteopathic; neuroprotective; nootropic; antipsoriatic;
KW   cerebroprotective; anticonvulsant; antidepressant; gene therapy;
KW   vaccine; autoimmune disorder; multiple sclerosis; allergic condition;
KW   insulin dependant diabetes; asthma; myeloid cell deficiency; ulcer;
KW   lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
KW   central nervous system disorder; Alzheimer's disease; stroke;
KW   Parkinson's disease; Huntington's disease; coagulation disorder;
KW   haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
KW   tumour; infection; depression; psoriasis; ss.
XX
OS   Mus musculus.
XX
SQ   WO200021991-A1.
XX
PD   20-APR-2000.
XX
PF   15-OCT-1999; 99WO-US24206.
XX
PR   15-OCT-1998; 98US-0104436.
XX
PA   (GEMV ) GENETICS INST INC.
XX
PI   Jacobs K, McCoy JM, LaValle ER, Collins-Racie LA, Evans C;
PI   Merberg D, Treacy M, Bowman MR;
XX
WPI: 2000-317938/27.
XX
PT   Isolated polynucleotides, and encoded proteins, comprising secreted
PT   expressed sequence tags (SESTs), useful for treating various disorders
PT   such as autoimmune, infectious, and central nervous system disorders -
XX
PS   Claim 1; Page 209; 803pp; English.
XX
CC   AAA43426 to AAA45925 represent specifically claimed secreted expressed
CC   sequence tags (SESTs), isolated from human, mouse, chicken and rat
CC   tissue sources. The SESTs can have a range of activities depending on
CC   the tissues they were isolated from. The activities include:

```



```

1 ThrProValSerGlnPheThrThrAlaAlaThrAlaSerValArgSerTh 17
|||||
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ID AAS70037 standard; cDNA; 6741 BP.

AC AAS70037:

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #5841.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.

OS Homo sapiens.

PN W0200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR P-PsDB; ABG05850.

XX

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity

PS Claim 1: SEQ ID No 5841: 103pp: English.

XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcr_sequences.

XX Sequence 6741 BP: 1764 A; 1725 C; 2134 G; 1117 T; 1 other;

alignment_scores:

Quality:	259.50	Length:	150
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US-09-786-130-1 x AAS70037/rev ..

Align seg 1/1 to reverse of: AAS70037 from: 1 to: 6741

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seq_documentation_block:

ID AA570676 standard; cDNA; 7103 BP.

AC AA570676;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #6480.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW Food supplement; medical imaging; diagnostic; genetic disorder; ss.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI: 2001-639362/73.

DR P-PSDB: ABG06489.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -

PS Claim 1; SEQ ID NO 6480; 103bp; English.

CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AA564197-AA594564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 7103 BP; 1879 A; 1805 C; 2233 G; 1185 T; 1 other;

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Quality: 259.50

Ratio: 3.089

Percent Similarity: 56.000

Length: 150

Gaps: 7

Percent Identity: 47.333

alignment_block:

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Align seg 1/1 to reverse of: AA570676 from: 1 to: 7103

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OM of: US-09-786-130-1 to: Issued_Patents_NA:* out_format : pfs
Date: Aug 19, 2002 11:55 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

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; GENERAL INFORMATION:  
; APPLICANT: Moyer, Richard W.  
; APPLICANT: Vi uela, Eladio  
; APPLICANT: Gibbs, E.P.J.  
; TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a  
; NUMBER OF INVENTIONS: 60  
; TITLE OF SEQUENCES: Live Vaccine Vector  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David R. Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: Florida  
; COUNTRY: U.S.A.  
; ZIP: 32606  
; COMPUTER READABLE FORM:  
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; COMPUTER: IBM PC compatible  
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; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/908,241  
; FILING DATE: 1-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/908,630  
; FILING DATE: 29-JUN-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/342,212  
; FILING DATE: 21-APR-1992  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saliwanchik, David R.  
; REGISTRATION NUMBER: 31,794  
; REFERENCE/DOCKET NUMBER: UF35.1.FWCC1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 904-375-8100  
; TELEFAX: 904-372-5800  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
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49      : APPLICANT: Vi uela, Eliadio
50      : APPLICANT: Gibbs, E.P.J.
51      : TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
52      : TITLE OF INVENTION: Live Vaccine Vector
53      : NUMBER OF SEQUENCES: 60
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55      CORRESPONDENCE ADDRESSES:
56      : ADDRESSEE: David R. SaliwanChik
57      : STREET: 2421 N.W. 41st street, Suite A-1
58      : CITY: Gainesville
59      : STATE: Florida
60      : COUNTRY: U.S.A.
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71      : FILING DATE:
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76      : FILING DATE: 1-JUL-1992

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NAME/KEY: CDS
LOCATION: 8215..8682
FEATURE:
NAME/KEY: CDS
LOCATION: 8715..9539
FEATURE:
NAME/KEY: CDS
LOCATION: 9562..10272
FEATURE:
NAME/KEY: CDS
LOCATION: 10316..11908
FEATURE:
NAME/KEY: CDS
LOCATION: 11971..12780
FEATURE:
NAME/KEY: CDS
LOCATION: 12829..13107
FEATURE:
NAME/KEY: CDS
LOCATION: 13149..14171
US-08-307-499-14

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alignment_scores:
Quality: 106.00      Length: 95
Ratio: 1.710        Gaps: 3
Percent Similarity: 65.263      Percent Identity: 28.421

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alignment_block:
US-09-786-130-1 x US-08-307-499-14 ..

Align seg 1/1 to: US-08-307-499-14 from: 1 to: 14176

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||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
7565 GTAAATGTAACGATATCTACGTAATCTAGATCTTATATGAT 7614
71 u.....GlyAsnGlySerPheIleGluHisLeuProGlyArgLeuTrpG 86
: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
7615 GGTAGTAAACAACATACATTCTGTGACACACTAAATAGCATATTATA 7664
86 IuGlySer.....ThrSerArgGluArgGlySerThrGlyThrGlnLeu 100
: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
7665 AAGAGAGAAATACATATCTACTGAAAAAATAGCATATGATTAAGTAA 7714
101 CysLysAlaLeuValLeuGlnLeuThrProAlaLeuHisSerThrAs 117
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
7715 CGTACGATCTTATATATATATATCTACGTCAGAAATGAGATGACAAA 7764
117 nPheSerCysValLeuValAspProGlnLeuValAlaGlnArgHisVal 134
: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
7765 ACTACATGTGTATATACGATATATACACACCTATCAAGGATCTATATA 7814
134 AlLeuAlaGlnLeuTyrPalaGlyLeuArgAlaThr 145
: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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7815 TATTAATTAATTATGAGGTGTTTAAATACTACA 7849
seq_name: /cgn2_6/ptodata/2/lna/6B_COMB.seq:US-09-299-268-1
seq_documentation_block:
; Sequence 1, Application US/09299268
; Patent No. 6217882
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Vi uela, Eladio
; APPLICANT: Gibbs, E.P.J.
; TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: U.S.A.
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,268
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/901,127
; FILING DATE:
; APPLICATION NUMBER: US 07/908,241
; FILING DATE: 1-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/908,630
; FILING DATE: 29-JUN-1992
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/342,212
; FILING DATE: 21-APR-1992
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF35.1.FWCI1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14176 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3852..4226
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 4585..4887
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 5131..5310
; FEATURE:
; NAME/KEY: CDS
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; FEATURE:
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; FEATURE:

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; NAME/KEY: CDS
; LOCATION: 10148..10513
; US-09-299-268-1

alignment_scores:
    Quality: 106.00      Length: 95
    Ratio: 1.710         Gaps: 3
    Percent Similarity: 65.263    Percent Identity: 28.421

alignment_block:
    US-09-786-130-1 x US-09-299-268-1/rev ..

Align seg 1/1 to reverse of: US-09-299-268-1 from: 1 to: 14176

57 ValAlaCysSerArgPheProAsn.....PheSerIleLeuTyrTrpLe 71
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6612 GTAAATGTACGATATCTAATCTTACGATATGATCTTATATTTGAT 6563
   71 u.....GlyAsnGlySerPheIleGluHisLeuProGlyArgLeuTrpG 86
   : ::::: |||::: |||::: |||::: |||::: |||::: |||:::
6562 GTAGGTACACACATTCATTCGTAGAACACATAATAGCATCATTTATA 6513
   : ::::: |||::: |||::: |||::: |||::: |||::: |||:::
86 LuGlySer.....ThrSerArgLuarGlySerThrGlyThrGlnLeu 100
   : ::::: |||::: |||::: |||::: |||::: |||::: |||:::
6512 AAGAGAGAAATACATAGTACTGAAAAAATGAGCATATGTATTAAGCTTA 6463
   : ::::: |||::: |||::: |||::: |||::: |||::: |||:::
101 CysLysAlaLeuValLeuGluGlnLeuThrProAlaLeuHisSerThrAs 117
   |||::: |||::: |||::: |||::: |||::: |||::: |||:::
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117 nPheSerCysValLeuValAspProGluGlnValValGlnArgHisValIv 134
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   : ::::: |||::: |||::: |||::: |||::: |||::: |||:::
134 AluValAlaGlnLeuTrpAlaGlyLeuArgAlaThr 145
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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-09-299-268-14

seq_documentation_block:
; Sequence 14, Application US/09299268
; Patent No. 6217882
; GENERAL INFORMATION:
; APPLICANT: Moyer, Richard W.
; APPLICANT: Vi uela, Eladio
; APPLICANT: Glibbs, E.P.J.
; TITLE OF INVENTION: Use of Recombinant Swine Poxvirus as a
; TITLE OF INVENTION: Live Vaccine Vector
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David R. Salivanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: U.S.A.
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,268
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/901,127
; FILING DATE:
; APPLICATION NUMBER: US 07/908,241
; FILING DATE: 1-JUL-1992
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 07/908,630
; FILING DATE: 29-JUN-1992
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/342,212
; FILING DATE: 21-APR-1992
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Salivanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF35.1.FWCC1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14176 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 138..1460
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2456..2659
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2809..3030
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3070..3330
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3356..4180
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 4392..5894
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 6171..6398
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APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1737 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: YES
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1737
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NAME/KEY: misc_feature
LOCATION: 342..343
OTHER INFORMATION: /note="splice junction"
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NAME/KEY: misc_feature
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OTHER INFORMATION: /note="splice junction"
US-09-173-151A-1

alignment_scores:
Quality: 96.50 Length: 126
Ratio: 1.322 Gaps: 7
Percent Similarity: 57.937 Percent Identity: 26.190

alignment_block:
US-09-786-130-1 x US-09-173-151A-1 ..

Align seg 1/1 to: US-09-173-151A-1 from: 1 to: 1737

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652 GTAGACGACAACTGAAATGAAAGTTACAGCTTACTACAGACAAAGCC 701
19 pProCysProSerGlnProProValPheProAlaAlaLysGlnCysProA 36
  ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
702 TCCC.....AAGCATTGTTCCCATGAGAAATCAGCCAAAGCTG 739
36 lalaGluValThrTrpProGluValGluValProLeuAsnGlyThrLeu 52
  :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
740 TTATAGATGTC.....CAGCTGGGTAGCCTCTGAAC..... 771
53 SerLeuSerCysValAlaCysSerArgPheProAsnPheser..... 66
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67 .....lLeuTyTrPLeuGlnGlyAsnGlySerPheIlleGlnHisLeuP 81
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810 TGGGCCAATGATCTACTGAGTGAAGAGAAAGTTATTATGAGAACTGG 859
81 roGlyArgLeuTrpGluGlySer.....ThrSerArgGluArgGly 94
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860 CAGGTCACTAGAGAAAGTGAATAAGCTTCTCAAGACACTCTTGA 909
95 SerThrGlyThrGlnLeuCysLysAlaLeuValLeuGlnGlnLeuThrPr 111
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910 GAAAGAGAGTGAATG.....GCACCTCATCTTGTGACTGAGTTGGGA 953
111 oAlaLeuHisSerThrAsnPheserCys 120
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seq_documentation_block:
; Sequence 3, Application US/09173151A
; Patent No. 6326472
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Debets, Johannes Eduard Maria
; APPLICANT: Antonius
; APPLICANT: Sana, Theodore R.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: Human Receptor Proteins: Related Reagents and Methods
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DMAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/173,151A
; FILING DATE: 14-OCT-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/065,776
; FILING DATE: 17-NOV-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/078,008
; FILING DATE: 12-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/081,883
; FILING DATE: 15-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/095,987

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; FILING DATE: 10-AUG-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/078,416
; FILING DATE: 18-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/062,066
; FILING DATE: 15-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0767X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ. ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2061 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2058
; US-09-173-151A-3

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alignment_scores:
  quality: 96.50      Length: 126
  ratio: 1.322        Gaps: 7
Percent Similarity: 57.937  Percent Identity: 26.190

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alignment_block:
US-09-786-130-1 x US-09-173-151A-3 ..

Align seq 1/1 to: US-09-173-151A-3 from: 1 to: 2061

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53 SerLeuSerCysValAlaCysSerArgPheProAsnPheser..... 66
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67 .....lLeuTyTrPLeuGlnGlyAsnGlySerPheIlleGlnHisLeuP 81
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825 TGGGCCAATGATCTACTGAGTGAAGAGAAAGTTATTATGAGAACTGG 874
81 roGlyArgLeuTrpGluGlySer.....ThrSerArgGluArgGly 94
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875 CAGGTCACTAGAGAAAGTGAATAAGCTTCTCAAGACACTCTTGA 924
95 SerThrGlyThrGlnLeuCysLysAlaLeuValLeuGlnGlnLeuThrPr 111
  :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
925 GAAAGAGAGTGAATG.....GCACCTCATCTTGTGACTGAGTTGGGA 968
111 oAlaLeuHisSerThrAsnPheserCys 120
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969 AGCT...GACCTGGCGAATTATACCTGC 993

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seq_name: /cgn2_6/ptodata/2/lna/5A_COMB.seq:US-08-145-006C-11

seq_documentation_block:
; Sequence 11, Application US/08145006C

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 20 oCysProSerGlnProProVal..... 27
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 537 GTGCCCCGTCGGGCGTCCGCTCTCATCGCTGTGTCCAGCGGAGGCA 568
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 587 TTCGTGCGCCGAGGCCCTTGTTGCCCTGCCCGCGAGCTTCACCCACG 636
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 637 GCTCCGCGAGACCCCTCGCGCGACCCCTATCTCAAGTGCGACCCACGAGAC 668

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58 AlaCysSerArgPheProAsnPheSerIleLeuTyrTrieu..... 71
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737 GATGGCCCTGAAACAGCTCGCCACAGCATCTGCTTGTGATCCCCCA 786
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72 .....GLYA 73
787 GATGTGAAGACCAAGCCCTGACCCCTCGCGGCTGTCGCGCCCATPCA 836
73 snGlySerPheIle.GluHisLeuProGlyArgLeuTrieuGlySerth 89
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89 rSerArgGluArgGlySerThrGlyThrGln.....LeuCysLysAlaL 104
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121 ValLeuValAspProGluGluValValGluArgHisValValLeuAlaG 137
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seq_documentation_block:
? Sequence 5, Application US/08466906B
? Patent No. 5849871
? GENERAL INFORMATION:
? APPLICANT: Cone, Roger D
? APPLICANT: Mountjoy, Kathleen G
? TITLE OF INVENTION: Melanocyte Stimulating Hormone Receptor
? TITLE OF INVENTION: and uses
? NUMBER OF SEQUENCES: 8
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
? STREET: 300 South Wacker Drive
? CITY: Chicago
? STATE: IL
? COUNTRY: USA
? ZIP: 60606
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/466,906B
? FILING DATE: 06-JUN-1995
? CLASSIFICATION: 530
? ATTORNEY/AGENT INFORMATION:
? NAME: No. 5849871nan, Kevin E
? REGISTRATION NUMBER: 35,303
? REFERENCE/DOCKET NUMBER: 92,154-H
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312-913-0001
? TELEFAX: 312-913-0002
? TELEX:
? INFORMATION FOR SEQ ID NO: 5:
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59 .....CysSerArgPheProAsnPheserIleLeuTyTrpLeug 72
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89 ThrSerArgGluArgGlySerThrGlyThrGlnLeuCysAlaLeuVal 105
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1135 ACA.....AGAGGCAGC.....GCCGGTCCACACGAGGCTTTGGC 1169
105 lLeuGlnGlnLeuThrProAlaLeuHisSerThrAsnPheserCysValL 122
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1170 CTTAAAGGCGCTGTCACTCACCATCTGCTGGCATTTTCTTCCTCTG 1219
122 euValAspProGlnValGlnArgHisValValLeuAlaGlnLeu 138
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1220 CTGGGCGCCCTTCTCTCGATCTCACACTCA..... 1251
139 TrpAlaGlyLeuArgAlaThrIleuProProThrGlnGlnAlaLeuPro 155
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1252 .....TCGTCTCTGCTGCCGAGCACCCGAGTGGCGCTGCATC 1289
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seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-201-746-5

seq_documentation_block:
: Sequence 5, Application US/09201746
: Patent No. 6268221
: GENERAL INFORMATION:
: APPLICANT: Cone, Roger D
: APPLICANT: Mountjoy, Kathleen G
: TITLE OF INVENTION: melanocyte Stimulating Hormone Receptor
: TITLE OF INVENTION: and Uses
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESSES:
: ADDRESSER: McDonnell Boehnen Hulbert & Berghoff
: STREET: 300 South Wacker Drive
: CITY: Chicago
: STATE: IL
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/201,746
: FILING DATE: 01-DEC-1998
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 6268221nan, Kevin E
: REGISTRATION NUMBER: 35,303
: REFERENCE/DOCKET NUMBER: 92,154-J
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-913-0001
: TELEFAX: 312-913-0002
: TELEX:

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: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1633 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA to mRNA
: FEATURE:
: NAME/KEY: 5'UTR
: LOCATION: 1..461
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 462..1415
: FEATURE:
: NAME/KEY: 3'UTR
: LOCATION: 1416..1633
: US-09-201-746-5

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alignment_scores:
  Quality: 93.50      Length: 171
  Ratio: 1.184      Gaps: 9
  Percent Similarity: 46.199      Percent Identity: 28.070

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alignment_block:
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US-09-786-130-1 x US-09-201-746-5 ..
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15 gSerThrLysAspProCys...ProSerGlnProProValAlaPheProAla 31
   |||
   |||||
939 CGGGCCCCGAGCCCTTGGCGGCATCTGGTGGCCAGTGTCTCTTCAG 988
31 lalysglnCysProAlaLeuGluValThrTrpProGluValGluValPro 47
   |||||
   |||||
989 CACGCTCTTCATCGGCTACTACACACCGTGGCCG..... 1023
48 LeuAsnGlyThrIleuSerIleuSerCysValAla..... 58
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1024 .....TCCTGCTGTGCTCTGCTGTCTTCCTTCG 1052
59 .....CysSerArgPheProAsnPheserIleLeuTyTrpLeug 72
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seq_name: /cgn2_6/prodata/2/ina/5b_COMB.seq:US-09-097-231-5
seq_documentation_block:
/ Sequence 5, Application US/09097231
/ Patent No. 6278038
/ GENERAL INFORMATION:
/ APPLICANT: Cone, Roger D
/ Chen, Wendiao
/ Low, Malcolm J
/ TITLE OF INVENTION: Mammalian Melanocortin Receptor and uses
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
/ STREET: 300 South Wacker Drive
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/097,231
/ FILING DATE: 12-Jun-1998
/ CLASSIFICATION: <unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 6278038nan, Kevin E
/ REGISTRATION NUMBER: 35,303
/ REFERENCE/DOCKET NUMBER: 96,886-C
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-913-0001
/ TELEFAX: 312-913-0002
/ TELEX: <unknown>
/ INFORMATION FOR SEQ ID NO: 5:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1633 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA to mRNA
/ FEATURE:
/ NAME/KEY: 5'UTR
/ LOCATION: 1..461
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 462..1415
/ FEATURE:
/ NAME/KEY: 3'UTR
/ LOCATION: 1416..1633
/ SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-097-231-5

alignment_scores:
Quality: 93.50 Length: 171
Ratio: 1.184 Gaps: 9
Percent Similarity: 46.199 Percent Identity: 28.070

alignment_block:
US-09-786-130-1 x US-09-097-231-5 ..

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GGGGGGCGCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 988
939 CGGGGGCGCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 988

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31 layslnclyproalaleuglvatlhtprprogivalaqlvalPro 47
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    48 leuAnSlYThrlleusertsercysVala..... 58
       |||||| | |
1024 ..... TCGTGCTGTGCCTGTGTCTTTCTTCTC 1052
      59 ..... CysSerArgPheProAsnPhseIleLeutYTrPrLeug 72
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1053 GCATGCTGTGTGCTGA... TGCGCGTGGCGAGCACGCCAAGTGTGCGCG 1099
      72 lYASngLySerPheIIeGIunISLueProGLyArGLeuTPrGLUGLySer 88
         ||::||| | | | | | |
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     89 ThSeSArgSLudargLySerThrGLyHrInGLneuCysLYSAleuVa 105
        ||| | | | | | | | :||| | | | | | | | | | |
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    139 TrPAIagILyeuARgAlathrlleuProPrrhgIngluaIaleuProSe 155
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    155 rSerHisSerSer 159
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1290 TTCAGAAGACTCA 1302

seq_name: /cgnt2_6/pltodata/2/lma/5B_COMB.seq;US-09-103-840A-2

seq_documentation_block:
; Sequence 2, Application US/09103840A
; Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

alignment_scores:
Quality: 87.00 Length: 176
Ratio: 1.208 Gaps: 8
Percent Similarity: 40.909 Percent Identity: 26.136

alignment_block:
US-09-786-130-1 x US-09-103-840A-2 ..

Align seg 1/1 to: US-09-103-840A-2 from: 1 to: 4403765
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seq_name: /cgn2_6/ptodata/2/lna/5A_COMB.seq:US-07-866-979-5
seq_documentation_block:
Sequence 5, Application US/07866979
Patent No. 5532347
GENERAL INFORMATION:
APPLICANT: Cone, Roger D
TITLE OF INVENTION: MountJoy, Kathleen G
TITLE OF INVENTION: Melanocyte Stimulating Hormone Receptor
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/866,979
FILING DATE: 19920410
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

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1  NAME: No. 5532347nan, Kevin E
2  REGISTRATION NUMBER: 35,303
3  REFERENCE/DOCKET NUMBER: 92,154
4  TELECOMMUNICATION INFORMATION:
5  TELEPHONE: 312-715-1000
6  TELEFAX: 312-715-1234
7  TELEX: 910-221-5317
8  INFORMATION FOR SEQ ID NO: 5:
9  SEQUENCE CHARACTERISTICS:
10 LENGTH: 1633 base pairs
11 TYPE: NUCLEIC ACID
12 STRANDEDNESS: single
13 TOPOLOGY: linear
14 MOLECULE TYPE: cDNA
15 FEATURE:
16 NAME/KEY: CDS
17 LOCATION: 462..1415
18 FEATURE:
19 NAME/KEY: 5'UTR
20 LOCATION: 1..461
21 FEATURE:
22 NAME/KEY: 3'UTR
23 LOCATION: 1416..1633
24 US-07-866-979-5
25
26 alignment_scores:
27     Quality: 85.50      Length: 171
28     Ratio: 1.110      Gaps: 9
29     Percent Similarity: 45.029      Percent Identity: 27.485
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31 alignment_block:
32 US-09-786-130-1 x US-07-866-979-5 ..
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34 Align seg 1/1 to: US-07-866-979-5 from: 1 to: 1633
35
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39 15 gserTrhLysAspProCys...ProSerGlnProProValPheProAla 31
40   ||:||||:||||| ||||| |||||
41 939 CGGGGCCCGCGACCGCTGGGGGCGCATGTGGGTGGCAGTGTGCTTCAG 988
42 31 lalysGlnCysProAlaLeuGluValThrTrpProGluValGluValPro 47
43   ||:||||:||||| :||| |||||
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58   ||||: |||:||||| |||||
59 1170 CTTAAAGGCGGTGTACCGCTCACACATCTGCTGGGCTTTTCTTCCTG 1219
60 122 euValAspProGluGlnValGlnArgHisValLeuAlaGlnLeu 138
61   ||||: |||:|||||
62 1220 CTGGGGCCCTTCTCTGCACTCACACCA..... 1251
63 139 TrpAlaGlyLeuArgAlaThrLeuProProThrGlnGlnAlaLeuPro 155

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1252 .....TCGTCCTGCCCCGAGACACCCCGTCGCGCTGCATC 1289
155 rSerHisSerSer 159
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